

GenCore version 5.1.6  
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OM protein - nucleic search, (using frame\_plus\_p2n model

Run on: September 7, 2005, 16:41:11; Search time 403 Seconds  
(without alignments)  
3938.433 Million cell updates/sec

Title: US-10-026-021-2  
Perfect score: 5078  
Sequence: 1 MATCGEXIEDPKVGNLGGK.....KLOCLSSILLMFNSPTPNFH 970

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
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-Q=/cgn2\_1/USPTO\_spool/US10026021/runat 07092005 174101 16170/app query.fasta 1.1159  
-DB=Issued Patents.NA -OFMT=fastap -SUPFIX=rni -MINMATCH=0.1 -LOOFC=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents.NA:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5075	99.9	3937	4	US-09-620-312D-280
2	3927.5	77.3	3447	1	Sequence 280, App
3	3927.5	77.3	3447	2	Sequence 3, Appli
4	1967	38.7	1600	1	Sequence 3, Appli
5	1967	38.7	1600	2	Sequence 5, Appli
6	1883.5	37.1	1453	1	Sequence 5, Appli
7	1883.5	37.1	1453	2	Sequence 1, Appli
8	590.5	11.6	2169	4	Sequence 1147, Ap
9	560.5	11.0	2070	2	Sequence 8, Appli
10	560.5	11.0	2770	3	Sequence 8, Appli
11	560.5	11.0	2789	3	Sequence 3, Appli
12	560.5	11.0	2789	3	Sequence 3, Appli

13	538.5	10.6	2783	3	US-09-136-282-1	Sequence 1, Appli
14	538.5	10.6	2783	3	US-09-505-744-1	Sequence 1, Appli
15	533	10.5	2124	3	US-09-198-122-1	Sequence 1, Appli
16	526.5	10.4	4557	3	US-09-614-221A-446	Sequence 446, App
17	510.5	10.1	2033	3	US-09-660-925B-10	Sequence 10, Appl
18	508.5	10.0	2198	2	US-08-755-728-2	Sequence 2, Appli
19	508.5	10.0	2198	2	US-08-974-655-2	Sequence 2, Appli
20	508.5	10.0	2198	3	US-09-283-011-2	Sequence 2, Appli
21	508.5	10.0	2198	4	US-09-012-135A-2	Sequence 2, Appli
22	508.5	10.0	2237	4	US-09-949-016-4590	Sequence 4590, Ap
23	508.5	10.0	2237	4	US-09-949-016-4591	Sequence 4591, Ap
24	508.5	10.0	2253	3	US-09-660-925B-3	Sequence 3, Appli
25	500	9.8	1539	4	US-09-633-328B-1	Sequence 1, Appli
26	492.5	9.7	2224	4	US-09-949-016-2384	Sequence 2384, Ap
27	492.5	9.7	2224	4	US-09-949-016-2385	Sequence 2385, Ap
28	489.5	9.6	1815	4	US-09-485-534-3	Sequence 3, Appli
29	487	9.6	2175	4	US-09-984-890-1	Sequence 1, Appli
30	487	9.6	2175	4	US-10-274-194-1	Sequence 1, Appli
31	485.5	9.6	1224	4	US-09-949-016-3955	Sequence 3955, Ap
32	485.5	9.6	1244	2	US-08-753-728-1	Sequence 1, Appli
33	485.5	9.6	1244	2	US-08-974-655-1	Sequence 1, Appli
34	485.5	9.6	1244	3	US-09-283-011-1	Sequence 1, Appli
35	485.5	9.6	1244	4	US-09-012-135A-1	Sequence 1, Appli
36	480	9.5	1281	2	US-09-016-000-7	Sequence 7, Appli
37	479.5	9.4	2950	4	US-09-949-016-1546	Sequence 1546, Ap
38	479.5	9.4	2950	4	US-09-949-016-1547	Sequence 1547, Ap
39	477.5	9.4	1791	4	US-09-270-767-1585	Sequence 1585, Ap
40	477.5	9.4	1791	4	US-09-270-767-17267	Sequence 17267, A
41	477	9.4	993	4	US-09-248-796A-4394	Sequence 4394, Ap
42	473	9.3	1929	3	US-09-359-161-4	Sequence 4, Appli
43	468	9.2	3246	4	US-09-614-221A-228	Sequence 228, App
44	465.5	9.2	2912	4	US-09-949-016-2363	Sequence 2363, Ap
45	465	9.2	2899	4	US-09-774-528-112	Sequence 112, App

#### ALIGNMENTS

RESULT 1  
US-09-620-312D-280  
; Sequence 280, Application US/09620312D  
; Patent No. 6569662  
; GENERAL INFORMATION:  
; APPLICANT: Fang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Reivan  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Zhou, Ping  
; APPLICANT: Ma, Yungqing  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: John Tillinghast  
; APPLICANT: Dmanac, Radoje T.  
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 784CIP2B  
; CURRENT APPLICATION NUMBER: US/09/620,312D  
; CURRENT FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 1105  
; SOFTWARE: pt\_FL\_genes Version 1.0  
; SEQ ID NO 280  
; LENGTH: 3937  
; TYPE: DNA



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Db 2374 AAATAGTGGCGAAATATCAATATATCTTCCAGGTTGTACAGCTTTGTAAGATCTAAATCT 2433

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Db 2434 CCCAAATCACTATTATACAGATATGCTAAATGCAATTTGATGGAGATTTCTCTGGT 2493

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Db 2494 GCTGATTTTGGGTTTGGTTTATGATGGGTAAATAATACAAACAGAGATTTTCATT 2553

Qy 741 GlnValIleGluLysThrGlyLysSerTyrThrLeuLysSerGluSerGluValAsnSer 760

Db 2554 CAGGTGATTGAAAGACAGGGAAGTCTTACACTTTTAAAAAGTGAAGTGAAGTTAATAGC 2613

Qy 761 LeuLysGluGluIleLysMetTyrMetAspHisAlaAsnGluGlyHisArgIleCysLeu 780

Db 2614 TTGAAGAGAGATAAATATGATGACCAATGCTAATGAGGTCATCGTATTGTGTTA 2673

Qy 781 AlaLeuGluSerIleLeuSerGluGluGluArgLysThrArgSerAlaProPhePhePro 800

Db 2674 GCATGGAAATCCATAATTTTCAAGACAGGAAAGAACTAGGAGTGTCTCTTTTCCCA 2733

Qy 801 IleIleIleGlyArgLysProGlySerThrSerProLysAlaLeuSerProProPro 820

Db 2734 ATAATCATAGGAAGAAACCTGGTAGTACTAGTTCACCTAAGGCGCTTATCACCTCTCT 2793

Qy 821 SerValAspSerAsnTyrProThrArgAspArgAlaSerPheAsnArgMetValMethHis 840

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Qy 861 LeuGlyLeuThrThrThrAlaSerGlyThrAspIleSerSerAsnSerLeuLysAspCys 880

Db 2914 CTGTGCTCTCAACTACAGCTCTTGGACAGACATCTCTTCTAATAGTCTAAAGATTTGT 2973

Qy 881 LeuProLysSerAlaGlnLeuLysSerValPheValLysAsnValGlyTrpAlaThr 900

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Qy 921 AlaGlyValSerSerIleSerTyrThrSerProAsnGlyGlnThrThrArgTyrGlyGlu 940

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Qy 961 MetPheSerAsnProThrProAsnPheHis 970

Db 3214 ATGTTTTCTAATCCGACTCTTAATTTTCAT 3243

RESULT 2

US-08-252-995D-3  
; Sequence 3, Application US/08252995D  
; Patent No. 5650501  
; GENERAL INFORMATION:  
; APPLICANT: Dennis, James W  
; APPLICANT: Heffernan, Mike

; APPLICANT: Fode, Carol  
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BERESKIN & PARR  
; STREET: 40 King Street West  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5H 3Y2  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/252,995D  
; FILING DATE: 02-JUN-1994  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kurdydk, Linda M  
; REGISTRATION NUMBER: 34,971  
; REFERENCE/DOCKET NUMBER: 3153-96  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 364-7311  
; TELEFAX: (416) 361-1398  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3447 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: Mus musculus  
; DEVELOPMENTAL STAGE: Lymphoid cDNA Library  
; IMMEDIATE SOURCE:  
; LIBRARY: Murine Lymphoid  
; CLONE: WGA-resistant chop clones  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: 1..205  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 206..2980  
; FEATURE:  
; NAME/KEY: 3'UTR  
; LOCATION: 2981..3447  
; US-08-252-995D-3

Alignment Scores:  
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Score: 3927.50 Matches: 763  
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Best Local Similarity: 78.58% Mismatches: 83  
Query Match: 77.34% Indels: 49  
DB: 1 Gaps: 9

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Db 266 GGATCATTTGCTGTGTCTACAGAGCTGAGTCCATACACTGGTTTGGAAAGTTGCAATC 325  
Qy 41 LysMetIleAspLysLysAlaMetTyrLysAlaGlyMetValGlnAtqValGlnAsnGlu 60  
Db 326 AAAATGATAGTAAAGAACCCATGTACAAAGCTGGAATGGTACAGAGAGTCCAAATGAG 385  
Qy 61 VallysIleHisCysGlnLeuLysHisProSerIleLeuGluLeuTyrAsnTyrPheGlu 80

Db 386 GTGAAATACATGTCAGTGAACACCCCTCTGCTTGGAGCTCTAATAATTACTTTGAA 445  
Qy AspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsnGlyGluMetAsnArgTyr 100  
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Qy LeuLysAsnArgValLysProPheSerGluAsnGluAlaArgHisPheMetHisGlnIle 120  
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Qy 221 AsnLysValValLeuAlaAspTyrGluMetProSerPheLeuSerIleGluAlaLysAsp 240  
Db 866 AACAAAGTAGTCTCGCAGATTATGAAATGCCAGCCTTTTGTCCACGAGAGGCCCGCAGGAC 925  
Qy 241 LeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeuSerLeuSerSerValLeu 260  
Db 926 CTTATCCACCACTTCTCGTAGAACCTCGCAGATCGGTTAAGTCTGCTCTCTGCTGTG 985  
Qy 261 AspHisProPheMetSerArgAsnSerSerThrLysSerLysAspLeuGlyThrValGlu 280  
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Qy 281 AspSerIleAspSerGlyHisAlaThrIleSerThrAlaIleThrAlaSerSerSerThr 300  
Db 1046 GACTCAATGGATAGTGGGCATGCTACACTTCCACAACAATTTACAGCCTCTCTGTTACC 1105  
Qy 301 SerIleSerGlySerLeuPheAspLysArgArgLeuLeuIleGlyGlnProLeuProAsn 320  
Db 1106 AGTTTGTAGGCGGCGCTACTTGAC---AGAAGACTTTTGGTTGGTCAACCACTTCCAAAT 1162  
Qy 321 LysMetThrValPheProLysAsnLysSerSerThrAspPheSerSerGlyAspGly 340  
Db 1163 AAAATTTACTGTATTTCAAAAAATAAAAAATTCAGTGACTTT---TCTTCAGGAGATGGA 1219  
Qy 341 AsnSerPheTyrThrGlnTyrGlyAsn-----GlnGluThrSerAsnSerGlyArgGly 358  
Db 1220 AGTAATTTTGTACTCAATGGGGAATCCAGAACGAAGAGCTAATAGTAGGGGAGCGGGG 1279  
Qy 359 ArgValIleGlnAspAlaGluArgProHisSerArgTyrLeuArgArgAlaTyrSer 378  
Db 1280 AGAGTGATTAAGATGCAGAGAGAGCGGCATTTCTCGATACCTCGCAGAGCTCTATCC 1339  
Qy 379 SerAspArgSerGlyThrSerAsnSerGlnSerGlnAlaLysThrTyrThrMetGluArg 398  
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Qy 399 CysHisSerAlaGluMetLeuSerValSerLysArgSerGlyGlyGluAsnGluGlu 418  
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Qy 419 ArgTyrSerProThrAspAsnAlaAsnIlePheAsnPhePheGlyLysThrSer 438

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Db 1436 -----CTGGATGAAATCAACACAGCTTCCAATCATCATGTGT 1471  
Qy 459 ProGlyLysThrProPheProPheAlaAspProThrProGlnThrGluThrValGlnGln 478  
Db 1472 CTAGGAAAAATCTCTTTTCCATTTTCAGACAGACACCTTCAGATGGAAATCGTACAGCAG 1531  
Qy 479 TrpPheGlyAsnLeuGlnIleAsnAlaHisLeuArgLysThrThrGluTyrAspSerIle 498  
Db 1532 TGGTTTGGGAATCTGCAAAATGAATGCTCATTTAGAGAAAATAATAGCACACACCGCTT 1591  
Qy 499 SerProAsnArgAspPheGlnGlyHisProAspLeuGlnLysAspThrSerLysAsnAla 518  
Db 1592 AGCCCAACACAGAGATTTCAGGACTATCCAGATTTTCAG---GACACGTTACGAAACGCT 1648  
Qy 519 TrpThrAspThrLysValLysLysAsnSerAspAlaSerAspAsnAlaHisSerValLys 538  
Db 1649 TGGACTGACAGAGAGCCAGCAGCAAGATGCTGATACTTCTGCCAATGTTTCATGCTGTGTAAG 1708  
Qy 539 GlnGlnAsnThrMetLysTyrMetThrAlaLeuHisSerLysProGluIleIleGlnGln 558  
Db 1709 CAGCTGAGTGCCTGAATATACATGAGTGCAATCACCATAAGCCTGAGGTTCATGCCACAG 1768  
Qy 559 GluCysValPheGlySerAspProLeuSerGluGlnSerLysThrArgGlyMetGluPro 578  
Db 1769 GAGCG-----GGCCTACATCTCTGAAACAAAGCAAGATAGAAATATGGAGTCG 1822  
Qy 579 ProTrpGlyTyrGlnAsnArgThrLeuArgSerIleThrSerProLeuValAlaHisArg 598  
Db 1823 ACCTGGGTTTACCAGAAACCTTACCTTAAGAAATATATACATCTCTCTGATGTCACAGA 1882  
Qy 599 LeuLysProIleAspGlnLysThrLysLysAlaValValSerIleLeuAspSerGluGlu 618  
Db 1883 TTAAGGCATATCAGACAGAAACCAAAAGGCTGTGTGAGCATCTTGTGATTCAGAGAG 1942  
Qy 619 ValCysValGluLeuValLysGluTyrAlaSerGlnGluTyrValLysGluValLeuGln 638  
Db 1943 GTGTGTGTGGAGCTTCTGAGAGAGTGTGCGTCTGAAAGGATATGTGAAAGAAAGTGTCTCAG 2002  
Qy 639 IleSerSerAspGlyAsnThrIleThrIleTyrTyrProAsnGlyGlyArgGlyPhePro 658  
Db 2003 ATATCGAGTGTGGGACTATGATCAGTCTTTATTTACCCGAACGATGGAAAGGCTTCTCT 2062  
Qy 659 LeuAlaAspArgProProSerProThrAspAsnIleSerArgTyrSerPheAspAsnLeu 678  
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Qy 719 ProGlyAlaAspPheGluValTyrPheTyrAspGlyValLysIleHisLysThrGluAsp 738  
Db 2243 CTTGGTGTGATTTGGAAGTTTGGTTTATGATGGAGCCAAATAATACATAAACTGAAAAAT 2302  
Qy 739 PheIleGlnValIleGluLysThrGlyLysSerTyrThrLeuLysSerGluSerGluVal 758  
Db 2303 TTAATTCACATAATTCAGAAAAACAGGGGATATCTTATAATTTAAAAAATGAAAAATGAAGTT 2362  
Qy 759 AsnSerLeuLysGluGluIleLysMetTyrMetAspHisAlaAsnGluGlyHisArgIle 778  
Db 2363 ACCAGCCTGAAAGAGGAAGTAAATATATATGACCAATGCTTAATGAGGGTCACCGTATT 2422  
Qy 779 CysLeuAlaLeuGluSerIleIleSerGluGluArgLysThrArgSerAlaProPhe 798  
Db 2423 TGCTTGTCACCTGGAAATCTGTAATCTCTGAGGAGGAAAGAGCAGGGGTTCTTCTTCATTTC 2482

QY 799 PheProIleIlelleGlyArgLysProGlySerThrSerSerProLysAlaLeuSerPro 818  
Db 2483 TTCCCTATAATCGTAGGAAGAAACCTGGTAATACTAGTTCCACCTAAAGCCCTATCAGCT 2542  
QY 819 ProProSerValAspSerAsnTyrProThrArgAspArgAlaSerPheAsnArgMetVal 838  
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QY 839 MetHisSerAlaAspSerProThrGlnAlaProIleLeuAsnProSerMetValThrAsn 858  
Db 2600 GTGAATAGTGGCGCTTCCACACAGTCCCGCAGGACTCAGTCTTCCACTGTGACAGTT 2659  
QY 859 GluGlyLeuGlyLeuThrThrAlaSerGlyThrAspIleSerSerAsnSerLeuLys 878  
Db 2660 GAAGGACTTGGCCACACAGCAGCTGCCACAGGACAGCGCTCTCTTCAAGT----- 2710  
QY 879 AspCysLeuProLysSerAlaGlnLeuLeuLysSerValPheValIysAsnValGlyTrp 898  
Db 2711 -----CTTCTTAATCTGCACAGCTTTTGAATCTGTTTTGTGAATAATGTTGGTGG 2764  
QY 899 AlaThrGlnLeuThrSerGlyAlaValTrpValGlnPheAsnAspGlySerGlnLeuVal 918  
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QY 919 ValGlnAlaGlyValSerSerIleSerTyrThrSerProAsnGlyGlnThrThrArgTyr 938  
Db 2825 GTCCAGGAGGAGTATCTTCCATCAGTTACACATCACCAGATGGTTCAGCAACTAGGTAT 2884  
QY 939 GlyGluAsnGluLysLeuProAspTyrIleLysGlnLysLeuGlnCysLeuSerIle 958  
Db 2895 GGAGAAATGAAATAATCCTGATACATCAACAGAAATACAGTGTCTTCTTCCATC 2944  
QY 959 LeuLeuMetPheSerAsnProThrProAsnPhe 969  
Db 2945 CTTCTGATGTTTCTTAATCCAACTCCTAATTT 2977

## RESULT 3

US-08-834-108-3  
; Sequence 3, Application US/08034108  
; Patent No. 5976893  
; GENERAL INFORMATION:  
; APPLICANT: Dennis, James W  
; APPLICANT: Heffernan, Mike  
; APPLICANT: Fode, Carol  
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BERESKIN & PARR  
; STREET: 40 King Street West  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5H 3Y2  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/834,108  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kurdydyk, Linda M  
; REGISTRATION NUMBER: 34,971  
; REFERENCE/DOCKET NUMBER: 3153-210  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 364-7311  
; TELEFAX: (416) 361-1398  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3447 base pairs

; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: Mus musculus  
; DEVELOPMENTAL STAGE: Lymphoid cDNA Library  
; IMMEDIATE SOURCE:  
; LIBRARY: Murine Lymphoid  
; CLONE: WGA-resistant chop clones  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: 1..205  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 206..2980  
; FEATURE:  
; NAME/KEY: 3'UTR  
; LOCATION: 2981..3447  
US-08-834-108-3

## Alignment Scores:

Pred. No.:	0	Length:	3447
Score:	3927.50	Matches:	763
Percent Similarity:	86.41%	Conservative:	76
Best Local Similarity:	78.58%	Mismatches:	83
Query Match:	77.34%	Indels:	49
DB:	2	Gaps:	9

US-10-026-021-2 (1-970) x US-08-834-108-3 (1-3447)

QY 1 MetAlaThrCysIleGlyLysIleGluSerPheLysValGlyAsnLeuLeuGlyLys 20  
Db 206 ATGGCGGCTGTCATCGGGAGAGGATCGAGACTTTAAAGTTGGAAATCTACTCGGTAAA 265  
QY 21 GlySerPheAlaGlyValTyrArgAlaGluSerIleHisThrGlyLeuGluValAlaIle 40  
Db 266 GGATCATTGCTGGTGTCTACAGAGCTGAGTCCATACACTGGTTTGGAGTTGCAATC 325  
QY 41 LysMetIleAspLysLysAlaMetTyrLysAlaGlyMetValGlnArgValGlnAsnGlu 60  
Db 326 AAATGATAGATAGAAAGCCATGTACAAAGCTGGAATGGTACAGAGAGTCCAAATGAG 385  
QY 61 ValLysIleHisCysGlnLeuLysHisProSerIleLeuGluLeuTyrAsnTyrPheGlu 80  
Db 386 GTGAAATATACATTGCCAGTTGCAACACCCCTCTGTCTTGGAGCTCTATAATTTACTTTGAA 445  
QY 81 AspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsnGlyGluMetAsnArgTyr 100  
Db 446 GATAACAATATGCTACTCGGTATTGGAATGTGCCACAATGGAGAAATGAACAGATAT 505  
QY 101 LeuLysAsnArgValLysProPheSerGluAsnGluAlaArgHisPheMetHisGlnIle 120  
Db 506 CTGAAGAACAGATAGAGCCCTTCTCAGAAAGGAGGAGTAGGACCTTCATGCACAGATT 565  
QY 121 IleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHisArgAspLeuThrLeuSer 140  
Db 566 ATCAGAGGAATGTTATATCTTCATCTCATGGCATAATGGACCGGAGCCTCACACTCTCT 625  
QY 141 AsnLeuLeuLeuThrArgAsnMetAsnIleLysIleAlaAspPheGlyLeuAlaThrGln 160  
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QY 161 LeuLysMetProHisGluLysHisTyrThrLeuCysGlyThrProAsnTyrIleSerPro 180  
Db 686 TTGAATATGCCACATGAAAGCACTATACACTCTGTGGGAGCTCTCTAATATATTTTACCA 745  
QY 181 GluIleAlaThrArgSerAlaHisGlyLeuGluSerAspValTrpSerLeuGlyCysMet 200  
Db 746 GAATTTGCACTCGAGTGCACATGGAGCTTGAATCTGTATATTTGGTCAATGGGCTGTATG 805  
QY 201 PheTyrThrLeuLeuIleGlyArgProPheAspThrValLysAsnThrLeu 220

Db 806 TCTTATACGTTACTTATTGGAGACCACTTTTGGACACTGACACAGTCAAGAACACATTG 865  
Qy 221 AsnLysValValLeuAlaAspTyrGluMetProSerPheLeuSerIleGluAlaLysAsp 240  
Db 866 AACAAAGTAGTCTCGGAGATATGAAATGCCAGCCTTTTGTCCAGGAGGCCCGCAGAC 925  
Qy 241 LeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeuSerLeuSerValLeu 260  
Db 926 CTTATCCACCGATTACTTCGTAGAAACCTCGAGATCGGTAAAGTCTGCTCTCTGTGTG 985  
Qy 261 AspHisProPheMetSerArgAsnSerSerThrLysSerLysAspLeuGlyThrValGlu 280  
Db 986 GACCATCTCTTCATGTCAGAAATCCTCCACAAAGAGTAAAGACGTAGGAGCTAGAG 1045  
Qy 281 AspSerIleAspSerGlyHisAlaThrIleSerThrAlaIleThrAlaSerSerThr 300  
Db 1046 GACTCAATGGTAGTGGGCATGCTACACTTCCACAACAATTTACAGCCCTCTCTGGTACC 1105  
Qy 301 SerIleSerGlySerLeuPheAspLysArgArgLeuLeuIleGlyGlnProLeuProAsn 320  
Db 1106 AGTTTGGTGGCAGCTACTTGAC---AGAAGACTTTTGGTTGGTCAACCACTTCCAAAT 1162  
Qy 321 LysMetThrValPheProLysAsnLysSerSerThrAspPheSerSerSerGlyAspGly 340  
Db 1163 AAAATTACTGTATTTCAAAAAATTAATAATTCAGTGACTTT---TCTTCAGGAGATCGA 1219  
Qy 341 AsnSerPheTyrThrGlnTrpGlyAsn-----GlnGluThrSerAsnSerGlyArgGly 358  
Db 1220 AGTAATTTTGTACTCAATGGGGAATCCAGAACAGAGCTAAATAGTAGGGGAGCGGG 1279  
Qy 359 ArgValIleGlnAspAlaGluGluArgProHisSerArgTyrLeuArgArgAlaTyrSer 378  
Db 1280 AGAGTGATTAAGATGCGAAGAGGCGGCATCTCGATACCTCGCAGAGCTCATTTCC 1339  
Qy 379 SerAspArgSerGlyThrSerAsnSerGlnSerGlnAlaLysThrTyrThrMetGluArg 398  
Db 1340 TCTGATAGCCAGCCCTCTTAAT---CAGTCTCGAGCAAAACATACTCAGTAGAACGT 1396  
Qy 399 CysHisSerAlaGluMetLeuSerValSerLysArgSerGlyGlyGluAsnGluGlu 418  
Db 1397 GTCACTCAGTAGAAATGTTTCAAAAGCCCTAGAGATCA----- 1435  
Qy 419 ArgTyrSerProThrAspAsnAsnAlaAsnIlePheAsnPhePheLysLysThrSer 438  
Db 1435 ----- 1435  
Qy 439 SerSerSerGlySerPheGluArgProAspAsnAsnGlnAlaLeuSerAsnHisLeuCys 458  
Db 1436 -----CTGGATGAAATCAACACAGTTCCCAATCATCTTGT 1471  
Qy 459 ProGlyLysThrProPheProPheAlaAspProThrProGlnThrGluThrValGlnGln 478  
Db 1472 CTAGAAAAACCTCTTTCCATTTGCAGACACAGACCTCGATGGAAATGGTACAGCAG 1531  
Qy 479 TrpPheGlyAsnLeuGlnIleAsnAlaHisLeuArgLysThrThrGluTyrAspSerIle 498  
Db 1532 TGGTTTGGGAATCTCGAATGAATGCTCATTTAGGAGAACTTAATGAGCACCACCGCTT 1591  
Qy 499 SerProAsnArgAspPheGlnGlyHisProAspLeuGlnLysAspThrSerLysAsnAla 518  
Db 1592 AGCCCCAACAGAGATTTCCAGGACTATCCAGATTTCAG---GACACGTTACGAACCGCT 1648  
Qy 519 TrpThrAspThrLysValLysLysAsnSerAspAlaSerAspAsnAlaHisSerValLys 538  
Db 1649 TGGAGTACACGAGCAGCAGCAAGAAATGCTGTACTTCTGCGCAATGTTTCATGCTGTAAG 1708  
Qy 539 GlnGlnAsnThrMetLysTyrMetThrAlaLeuHisSerLysProGluIleIleGlnGln 558  
Db 1709 CAGCTGAGTGCATGAAATACATGATGTCATCATCCATAGCCCTGAGGTCATGCCACAG 1768  
Qy 559 GluCysValPheGlySerAspProLeuSerGluGlnSerLysThrArgGlyMetGluPro 578  
Db 1769 GAGCCG-----GGCCTACATCTCTATCTGAAACAAAGCAAGAAATAGAGTATGGAGTCG 1822

Qy 579 ProTrpGlyTyrGlnAsnArgThrIleuArgSerIleThrSerProLeuValAlaHisArg 598  
Db 1823 AACTGGGTTTACCAGAAACCTTACCTTAAGAAGTATTACATCTCTCTGATTGCTCACAGA 1882  
Qy 599 LeuLysProIleArgGlnLysThrLysLysAlaValValSerIleLeuAspSerGluGlu 618  
Db 1883 TTAAGCCCATCAGACAGAAACCAAAAGGCTGTGGTGGACATCTTGTATTTCAGAGAG 1942  
Qy 619 ValCysValGluLeuValLysGluTyrAlaSerGlnGlnTyrValLysGluValLeuGln 638  
Db 1943 GTGTGTGTGGAGCTTCTGAGAGAGTGTGCGTCTGAAGGATATGTGAAGAAGTGTCTTCCAG 2002  
Qy 639 IleSerSerAspGlyAsnThrIleThrIleTyrTyrProAsnGlyGlyArgGlyPhePro 658  
Db 2003 ATATCGAGTGTATGGGACTATGATCACTGTTTATTACCCGAACGATGGGAAGGCTTTCCT 2062  
Qy 659 LeuAlaAspArgProSerProThrAspAsnIleSerArgTyrSerPheAspAsnLeu 678  
Db 2063 CTTGCTGACAGACCTCCCTTCCCTACTGACAAACATCAGTAGGTACAGCTTTTGACAATCTA 2122  
Qy 679 ProGluLysTyrTrpArgLysTyrGlnTyrAlaSerArgPheValGlnLeuValArgSer 698  
Db 2123 CCAGAAAAATACTGGCGGAATATACGATATGCTTCCAGATTCATTACGTAGTAAGATCT 2182  
Qy 699 LysSerProLysIleThrTyrPheThrArgTyrAlaLysCysIleLeuMetGluAsnSer 718  
Db 2183 AAAATCCCAAAATCACTTATTTTACAAGATATGCTAAATGTATTTTGTATGGAATAATCT 2242  
Qy 719 ProGlyAlaAspPheGluValTrpPheTyrAspGlyValLysIleHisLysThrGluAsp 738  
Db 2243 CCTGGTGTGATTTGGAAGTGTGGTTTATGATGGCCAAAATACATAAACCTGAAAAAT 2302  
Qy 739 PheIleGlnValIleGluLysThrGlyLysSerTyrThrLeuLysSerGluSerGluVal 758  
Db 2303 TTAATTCACATAATTTGAGAAAAACAGGATATCTTTAATTTAAAAAATGAAAAATGAAGTT 2362  
Qy 759 AsnSerLeuLysGluGluIleLysMetTyrMetAspHisAlaAsnGluGlyHisArgIle 778  
Db 2363 ACCAGCCTGAAAGAGGAAGTAAAGATATATATGACCATTGCTAATGAGGGTCACTGATT 2422  
Qy 779 CysLeuAlaLeuGluSerIleLeuSerGluGluArgLysThrArgSerAlaProPhe 798  
Db 2423 TGCCTTGACCTGGAAATCTGTAATCTCTGAGGAGGAAGAGAGGCGGTCTTCAATC 2482  
Qy 799 PheProIleIleIleGlyArgLysProGlySerThrSerSerProLysAlaLeuSerPro 818  
Db 2483 TTCCCTATAATCGTAGGAAGAAAAACCTGGTAATACTAGTTCCACCTAAAGCCTTATCAGCT 2542  
Qy 819 ProProSerValAspSerAsnTyrProThrArgAspArgAlaSerPheAsnArgMetVal 838  
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Qy 839 MethHisSerAlaAlaSerProThrGlnAlaProIleLeuAsnProSerMetValThrAsn 858  
Db 2600 GTGAATAGTCGCGCTTTCCCCACACAGTCCCCAGAGACTCAGTCTCTTCCACTGTGACGTT 2659  
Qy 859 GluGlyLeuGlyLeuThrThrAlaSerGlyThrAspIleSerSerAsnSerLeuLys 878  
Db 2660 GAAGGACTTGGCCACACAGCGACTGCCACAGAACAGGCGTCTCTCAAGT----- 2710  
Qy 879 AspCysLeuProLysSerAlaGlnLeuLysSerValPheValLysAsnValGlyTrp 898  
Db 2711 -----CTTCCATAATCTGCACAGCTTTTGAATCTGTGTTTTGTGAAAAATGTTGGTTGG 2764  
Qy 899 AlaThrGlnLeuThrSerGlyAlaValTrpValGlnPheAsnAspGlySerGlnLeuVal 918  
Db 2765 GCTACACAGCTTAAGTACCGAGCTGTGGGTTTCAAGTTAATGATGGGTTCACGTTGTT 2824  
Qy 919 ValGlnAlaGlyValSerSerIleSerTyrThrSerProAsnGlyGlnThrThrArgTyr 938  
Db 2825 GTCCAGGAGGAGTATCTTCCATCAGTTACACATCACAGATGCTGACAACTAGGTAT 2884



QY 939 GlyGluAsnGluLysLeuProAspTyrIleLysGlnLysLeuGlnCysLeuSerSerIle 958  
 Db 2885 GGAGAAAATGAATAATACCTGAATACATCAACAGAAATTACAGTGCTTCTTCCATC 2944  
 QY 959 LeuLeuMetPheSerAsnProThrProAsnPhe 969  
 Db 2945 CTTCTGATGTTTCTTAATCCAACTCCTAATTTT 2977

RESULT 4  
 US-08-252-995D-5  
 ; Sequence 5, Application US/08252995D  
 ; Patent No. 5650501  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dennis, James W  
 ; APPLICANT: Heffernan, Mike  
 ; APPLICANT: Fode, Carol  
 ; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BERESKIN & PARR  
 ; STREET: 40 King Street West  
 ; CITY: Toronto  
 ; STATE: Ontario  
 ; COUNTRY: Canada  
 ; ZIP: M5H 3Y2

COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/252,995D  
 ; FILING DATE: 02-JUN-1994  
 ; CLASSIFICATION: 536  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Kurdydyk, Linda M  
 ; REGISTRATION NUMBER: 34, 971  
 ; REFERENCE/DOCKET NUMBER: 3153-96  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (416) 364-7311  
 ; TELEFAX: (416) 361-1398  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1600 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear

MOLECULE TYPE: cDNA  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Mus musculus  
 ; DEVELOPMENTAL STAGE: Lymphoid cDNA Library  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: Murine lymphoid  
 ; CLONE: WGA-resistant chop clones  
 ; FEATURE:  
 ; NAME/KEY: 5'UTR  
 ; LOCATION: 1..205  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 206..1597  
 US-08-252-995D-5

Alignment Scores:  
 Pred. No.: 8,72e-192 Length: 1600  
 Score: 1967.00 Matches: 385  
 Percent Similarity: 92.0% Conservative: 34  
 Best Local Similarity: 84.62% Mismatches: 30  
 Query Match: 38.74% Indels: 7  
 Ds: 1 Gaps: 5

US-10-026-021-2 (1-970) x US-08-252-995D-5 (1-1600)

QY 1 MetaAlaThrCysIleGlyGluLysIleGluAspPheLysValGlyAsnLeuLeuGlyLys 20

Db 206 ATGGCGGCGTGCATCGGGGAGGATCGAGGACTTTAAAGTTGGAAATCTACTCGGTAAA 265  
 QY 21 GlySerPheAlaGlyValTyrArgAlaGluSerIleHisThrGlyValGluValAlaIle 40  
 Db 266 GGATCAATTTGCTGGTGTCTACAGAGCTGAGTCCATACACACTGGTTTGGAGTTCAATC 325  
 QY 41 LysMetIleAspLysLysAlaMetTyrLysAlaGlyMetValGlnArgValGlnAsnGlu 60  
 Db 326 AAAATGATAGATAAGAAAGCCATGTACAAAGCTGGAATGGTACAGAGAGTCCAAATGAG 385  
 QY 61 ValIysIleHisCysGlnLeuLysHisProSerIleLeuGluLeuTyrAsnTyrPheGlu 80  
 Db 386 GTGAAAATACATTCGCCAGTTGAAACACCCCTCTGTCTTGGAGCTCTATAATTAATTTGAA 445  
 QY 81 AspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsnGlyGluMetAsnArgTyr 100  
 Db 446 GATAACAATTAATGTCTACCTGGTATTGGAAATGTGCCCAATGGAGAAATGAACAGATAT 505  
 QY 101 LeuLysAsnArgValLysProPheSerGluAsnGluAlaArgHisPheMetHisGlnIle 120  
 Db 506 CTGAAGAACACAGATGAGCCCTTTCTCAGAAAGGGAAGCTAGGCACCTTCATGCACCAGATT 565  
 QY 121 IleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHisArgAspLeuThrLeuSer 140  
 Db 566 ATCAGAGGAATGTTATATCTTCATTCATGGCATATTGCACCGGAGCCTCACACTCTCT 625  
 QY 141 AsnLeuLeuLeuThrArgAsnMetAsnIleLysIleAlaAspPheGlyLeuAlaThrGln 160  
 Db 626 AACATCTTACTTACGGGAAATATGAACATAAAATTTGCTGACTTTGGACTAGCAACGAG 685  
 QY 161 LeuLysMetProHisGluLysHisTyrThrLeuCysGlyThrProAsnTyrIleSerPro 180  
 Db 686 TTGAATATGCCACATGAAAGACCATATACACTCTGTGGGACTCTCTAATATATATTTACCA 745  
 QY 181 GluIleAlaThrArgSerAlaHisGlyLeuGluSerAspValTrpSerLeuGlyCysMet 200  
 Db 746 GAAATTCACACTCGAAGTGCACTGGACTTGAATCTGTATTTGGTTCATTTGGGCTGTATG 805  
 QY 201 PheTyrThrLeuLeuIleGlyArgProPheAspThrAspThrValLysAsnThrLeu 220  
 Db 806 TCTTATAGTTTACTTATTGGGAAGACCACCTTTTGACACTGACACAGTCAAGAAGACATG 865  
 QY 221 AsnLysValValLeuAlaAspTyrGluMetProSerPheLeuSerIleGluAlaLysAsp 240  
 Db 866 AACAAAGTAGTCTGGCAGATTATGAATGCCAGCCTTTTGTCCAGAGAGGCCCCAGGAC 925  
 QY 241 LeuIleHisGlnLeuLeuArgAsnProAlaAspArgLeuSerLeuSerSerValLeu 260  
 Db 926 CTTATCCACCAAGTTACTTCGTAGAAACCTTCAGATCGGTTAAGTCTCTCTCTGTGTG 985  
 QY 261 AspHisProPheMetSerArgAsnSerSerThrLysSerLysAspLeuGlyThrValGlu 280  
 Db 986 GACCATCTTTTCATGTACGAAATCTTCCAAAGAGTAAGACGTAGGAGCTGTAGAG 1045  
 QY 281 AspSerIleAspSerGlyHisAlaThrIleSerThrAlaIleThrAlaSerSerSerThr 300  
 Db 1046 GACTCAATGGATAGTGGGCATGCTACATTTCCACAAACAAATTAACAGCTCTTCTGTGATC 1105  
 QY 301 SerIleSerGlySerLeuPheAspLysArgArgLeuLeuIleGlyGlnProLeuProAsn 320  
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 QY 321 LysMetThrValPheProLysAsnLysSerSerThrAspPheSerSerSerGlyAspGly 340  
 Db 1163 AAAATTAATGTTATTTCAAAAATAATAATAATTAATTAATTAATTAATTAATTAATTAAT 1219  
 QY 341 AsnSerPheTyrThrGlnTyrGlyAsn-----GlnGluThrSerAsnSerGlyArgGly 358  
 Db 1220 AGTAATTTTGTACTCAATGGGGAATCCAGAACAGAGAGCTAATAGTAGGGGACGGGG 1279  
 QY 359 ArgValIleGlnAspAlaGluArgProHisSerArgTyrLeuArgArgAlaTyrSer 378

Db 1280 AGAGTGATTGAAGATGCAGAGAGAGCGCGCATTCCTCGATCTCGCGAGAGCTCATTC 1339  
Qy 379 SerAspArgSerGlyThrSerAsnSerGlnAlaLysThrTyrThrMetGluArg 398  
Db 1340 TCTGATAGAGCCGCCCTCTTAAT---CAGTCTCGAGCAAAACATACCTAGTAGACGT 1396  
Qy 399 CysHisSerAlaGluMetLeuSerValSerLysArgSerGlyGlyGlyGluAsnGlu 418  
Db 1397 TGTCACTCAGTAGAATGCTTTCAAGCGCTAGAGATCA---CTGGATGAAATCAACAC 1453  
Qy 419 ArgTyrSerProThrAspAsnAlaAsnIlePheAsnPhePheLysGluLysThrSer 438  
Db 1454 AGGTATTCAACCCACCAAGCAATGCTCAATGT-TTTAACTTCATTAAACACCAACAGCC 1512  
Qy 439 SerSerSerGlySerPheGluArgProAspAsnGlnAlaLeu 453  
Db 1513 AATAGTTAAGGATCTTTTGAAGACCGGTATATGACTGAGCAGTA 1557

## RESULT 5

US-08-834-108-5  
; Sequence 5, Application US/08834108  
; Patent No. 5976893  
; GENERAL INFORMATION:  
; APPLICANT: Dennis, James W  
; APPLICANT: Heffernan, Mike  
; APPLICANT: Fode, Carol  
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BERESKIN & PARR  
; STREET: 40 King Street West  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5H 3Y2  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/834,108  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kurydyk, Linda M  
; REGISTRATION NUMBER: 34,971  
; REFERENCE/DOCKET NUMBER: 3153-210  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 364-7311  
; TELEFAX: (416) 361-1398  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1600 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: Mus musculus  
; DEVELOPMENTAL STAGE: Lymphoid cDNA Library  
; IMMEDIATE SOURCE:  
; LIBRARY: Murine Lymphoid  
; CLONE: WGA-resistant chop clones  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: 1..205  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 206..1597  
US-08-834-108-5

Alignment Scores:

Pred. No.:	8.72e-192	Length:	1600
Score:	1967.00	Matches:	385
Percent Similarity:	92.09%	Conservative:	34
Best Local Similarity:	84.62%	Mismatches:	30
Query Match:	38.74%	Indels:	7
DB:	2	Gaps:	5

US-10-026-021-2 (1-970) x US-08-834-108-5 (1-1600)

Qy	1	MetAlaThrCysIleGlyGluLysValGlyAsnLeuGlyLys	20
Db	206	ATGCGCGGTCATCGGAGAGGATCGAGACTTTAAGGTTGGAATCTACTCGGTAA	265
Qy	21	GlySerPheAlaGlyValTyrArgAlaGluSerIleHisThrGlyLeuGluValAlaIle	40
Db	266	GGATCATTTGCTGTCTTACAGAGCTGAGTCCATACACACTGGTTTGGAAAGTTGCAATC	325
Qy	41	LysMetIleLeuLysAlaMetTyrLysAlaGlyMetValGlnArgValGlnAsnGlu	60
Db	326	AAAATGATAGATAAGAAGCCATGTACAAAGCTGGAATGGTACAGAGAGTCCAAATGAG	385
Qy	61	ValLysIleHisCysGlnLeuLysHisProSerIleLeuGluLeuTyrAsnTyrPheGlu	80
Db	386	GTGAAATACATTGCCAGTTGAAACACCCCTCTCTCTTGGAGCTCTATAATTTACTTTGAA	445
Qy	81	AspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsnGlyGluMetAsnArgTyr	100
Db	446	GATAACAATTTATGCTACTCTGTTTGAATGTGCCACAATGGAGAAATGAACAGATAT	505
Qy	101	LeuLysAsnArgValLysProPheSerGluAsnGluAlaArgHisPheMetHisGlnIle	120
Db	506	CTGAAGAACAGATGAAGCCCTTCTCAGAAAGGGAAGCTAGGCACCTTCATGCCAGATT	565
Qy	121	IleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHisArgAspLeuThrLeuSer	140
Db	566	ATCACAGGAATGTTATATCTTCATCTCATGGCATATTCACCGGAGCTTCACACTCTCT	625
Qy	141	AsnLeuLeuThrArgAsnMetAsnIleLysIleAlaAspPheGlyLeuAlaThrGln	160
Db	626	AACATCTTACTTACGCGGAATATGAACATAAAATTTGCTGACTTTGGACTAGCAACGAG	685
Qy	161	LeuLysMetProHisGluLysHisTyrThrLeuCysGlyThrProAsnTyrIleSerPro	180
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Qy	181	GluIleAlaThrArgSerAlaHisGlyLeuGluSerAspValTrpSerLeuGlyCysMet	200
Db	746	GAAATTCGAACCTCGAAGTGCACATGGACTTGAATCTGATATTTGGTCATTGGGCTGTATG	805
Qy	201	PheTyrThrLeuLeuIleGlyArgProPheAspThrAspThrValLysAsnThrLeu	220
Db	806	TCATTATAGTTACTTTATTGGAAGACCACTTTTGACACTGCACAGTCAAGAACACATTG	865
Qy	221	AsnLysValValLeuAlaAspTyrGluMetProSerPheLeuSerIleGluAlaLysAsp	240
Db	866	AACAAGTAGTCTCGCAGATTATGAATGCCAGCTTTTGTACGAGAGGCCCGAGAC	925
Qy	241	LeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeuSerLeuSerSerValLeu	260
Db	926	CTTATCCACCAAGTTACTTCGTAGAAACCCCTGCAGATCGGTTAAGTCTCTCTCTGTGTG	985
Qy	261	AspHisProPheMetSerArgAsnSerSerThrLysSerLysAspLeuGlyThrValGlu	280
Db	986	GACCATCTTTTCATGTCTACGAAATCCCTTCACCAAGAGATAAGAGCTGAGGAGCTGTAG	1045
Qy	281	AspSerIleAspSerGlyHisAlaThrIleSerThrAlaIleThrAlaSerSerThr	300
Db	1046	GACTCAATGGATAGTGGCATGCTACATTTCCACCAACAAATTACAGCCTCTTCTGTTACC	1105
Qy	301	SerIleSerGlySerLeuPheAspLysArgArgLeuLeuIleGlyGlnProLeuProAsn	320
Db	1106	AGTTTGTAGTGGCAGCTACTTGTAC---AGAAGACTTTTGTGGTGGTCAACCACTTCCAAAT	1162



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QY 321 LysMetThrValPheProLysAsnLysSerSerThrAspPheSerSerSerGlyAspGly 340
Db 1163 AAAATTACTGTATTTTCAAAAAATAAAATTCAGTGACTTT---TCITCAGGAGATGGA 1219
QY 341 AsnSerPheTyrThrGluTyrGlyAsn-----GlnGluThrSerAsnSerGlyArgGly 358
Db 1220 AGTAATTTTGTACTCAATGGGGAATCCAGAACGAAGAGCTTAATAGTAGGGGCGGGGG 1279
QY 359 ArgValIleGlnAspAlaGluArgProHisSerArgTyrLeuArgAlaTyrSer 378
Db 1280 AGAGTGATTGAAGATGCAGAGAGAGCGCATTCCTCGATACCTCGCGAGAGCTCATTC 1339
QY 379 SerAspArgSerGlyThrSerAsnSerGlnSerGlnAlaLysThrTyrThrMetGluArg 398
Db 1340 TCTGATAGAGCCAGCCCTCTTAAT---CAGTCTCAGCAAAAACATACCTCAGTAGAAGCT 1396
QY 399 CysHisSerAlaGluMetLeuSerValSerLysArgSerGlyGlyGluAsnGlu 418
Db 1397 TGTCACTCAGTAGAATGCTTTCAAGCCTAGAGATCA---CTGGATGAAATCAACAC 1453
QY 419 ArgTyrSerProThrAspAsnAlaAsnIlePheAsnPhePheLysGluLysThrSer 438
Db 1454 AGGTATTCAACCAACCAAGCAATGTCATGT-TTTAACTTCATTAAACACCAACAGCC 1512
QY 439 SerSerSerGlySerPheGluArgProAspAsnAsnGlnAlaLeu 453
Db 1513 AATAGTTAAGGATCTTTTGAAGACCGTATTAATGACTGAGCAGTA 1557
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## RESULT 6

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US-08-252-995D-1
; Sequence 1, Application US/08252995D
; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3V2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1453 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; DEVELOPMENTAL STAGE: Lymphoid cDNA Library
; IMMEDIATE SOURCE:
; LIBRARY: Murine Lymphoid
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## CLONE: WGA-Resistant Chop Clones

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 206..1453
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..205
US-08-252-995D-1
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## Alignment Scores:

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Pred. No.: 2,85e-183 Length: 1453
Score: 1883.50 Matches: 362
Percent Similarity: 94.19% Conservative: 27
Best Local Similarity: 87.65% Mismatches: 19
Query Match: 37.09% Indels: 5
DB: 1 Gaps: 4
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US-10-026-021-2 (1-970) x US-08-252-995D-1 (1-1453)

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QY 1 MetAlaThrCysIleGlyGluLysValGlyAsnLeuGlyLys 20
Db 206 ATGGCGCGTGCATCGGGGAGGATCGAGGACTTTAAAGTTGGAAATCTACTCGGTAAA 265
QY 21 GlySerPheAlaGlyValTyrArgAlaGluSerIleHisThrGlyLeuGluValAlaIle 40
Db 266 GGATCATTTGCTGCTGTCTACAGAGCTGAGTCCATACACACTGGCTTTGGAAGTTGCAATC 325
QY 41 LysMetIleAspLysLysAlaMetTyrLysAlaGlyMetValGlnArgValGlnAsnGlu 60
Db 326 AAAATGATAGATAAGAAGCCATGTACAAAGCTGGAATGGTACAGAGAGTCCAAAATCAG 385
QY 61 ValLysIleHisCysGlnLeuLysHisProSerIleLeuGluLeuTyrAsnTyrPheGlu 80
Db 386 GTGAAATACATTCAGTTCAGTTCGAAACACCCCTCTGCTTGGAGCTCTATAATTACTTGA 445
QY 81 AspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsnGlyGluMetAsnArgTyr 100
Db 446 GATAACAATTTATGCTACCTGGTATTGGAATGTGCCAATGTGCCAATGGAGAAATGAACAGAT 505
QY 101 LeuLysAsnArgValLysProPheSerGluAsnGluAlaArgHisPheMetHisGlnIle 120
Db 506 CTGAAGAACAGAAATGAAGCCCTTTCTCAGAAAGGAAAGCTAGGCACCTTCATGCACAGATT 565
QY 121 IleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHisArgAspLeuThrLeuSer 140
Db 566 ATCACAGAAATGTTATATCTTCATTCATGGCATATTGCCCGGACCTCACACTCTCT 625
QY 141 AsnLeuLeuThrArgAsnMetAsnIleLysIleAlaAspPheGlyLeuAlaThrGln 160
Db 626 AACATCTTACTTACGCGGAATATGAACATAAAATTTGCTGACTTTGGACTAGCAACGCGAG 685
QY 161 LeuLysMetProHisGluLysHisTyrThrLeuCysGlyThrProAsnTyrIleSerPro 180
Db 686 TTGAATATGCCACATGAAGACACTATACACTCTGTGGGACTCCTAATATTATATTTCACCA 745
QY 181 GluIleAlaThrArgSerAlaHisGlyLeuGluSerAspValTyrSerLeuGlyCysMet 200
Db 746 GAAATTCGAATCTGAAGTGCACATGGACTTGAATCTGATATTGCTCATTTGGGCTGTATG 805
QY 201 PheTyrThrLeuLeuIleGlyArgProPheAspThrAspThrValLysAsnThrLeu 220
Db 806 TCTTATACGTTACTTATTGGAAGACCACTTTTGACACTGCACACAGTCAAGAACACATTG 865
QY 221 AsnLysValValLeuAlaAspTyrGluMetProSerPheLeuSerIleGluAlaLysAsp 240
Db 866 AACAAAGTAGTCTCTGGCAGATTTATGAAATGCGACCTTTTGTCCAGAGAGGCCGAGGAC 925
QY 241 LeuIleHisGlnLeuLeuArgAsnProAlaAspArgLeuSerLeuSerValLeu 260
Db 926 CTTATCCACCAAGTTACTTCGTAGAAACCTCCACATCGTGAAGTCTGCTCTCTCTGTGTG 985
QY 261 AspHisProPheMetSerArgAsnSerSerThrLysSerLysAspLeuGlyThrValGlu 280
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Db 986 GACCATCTTTTCATGTCACGAAATCCTTCCACCAAGAGTAAAGACGTAGGACGTGTAGAG 1045
Qy 281 AspSerIleAaspSerGlyHisIaThrIleSerThrAlaIleThrAlaSerSerSerThr 300
Db 1046 GACTCAATGGATAGTGGGCATCTACACTTTCACACAAATTTACAGCCTCTTCTGGTACC 1105
Qy 301 SerIleSerGlySerLeuPheAaspLysArgArgLeuLeuIleGlyGlnProLeuProAan 320
Db 1106 AGTTTGAGTGGCAGCTACTTGAC---AGNAGACTTTTGGTGGTCAACCACTTCCAAT 1162
Qy 321 LysMetThrValPheProLysAsnLysSerSerThrAspPheSerSerSerGlyAaspGly 340
Db 1163 AAAATTTACTGTATTTCAAAAAATAAAATTCAGTGACTTT---TCTTCAGGAGATGGA 1219
Qy 341 AsnSerPheTyThrGlnTrpGlyAan-----GlnGluThrSerAsnSerGlyArgGly 358
Db 1220 AGTAATTTTGTACTCAATGGGGAATCCAGAACCAAGAGCTAATAGTAGGGGACGGGG 1279
Qy 359 ArgValIleGlnAspAlaGluArgProHisSerArgTyThrLeuArgArgAlaTySer 378
Db 1280 AGAGTGATGAGATGCGAAGAGAGCGCGCATTTCTCGATACCTCGCGAGACTCATTC 1339
Qy 379 SerAspArgSerGlyThrSerAsnSerGlnSerGlnAlaLysThrTyThrMetGluArg 398
Db 1340 TCTGATAGACGAGCCCTCTAAT---CAGTCTCGAGCAAAAACATACCTCAGTAGAACGT 1396
Qy 399 CysHisSerAlaGluMetLeuSerValSerLysArgSer 411
Db 1397 TGTCACTCAGTAGAATGCTTTTCAAGCCCTAGAAGATCA 1435
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## RESULT 7

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US-08-834-108-1
; Sequence 1, Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESS: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,108
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurodyck, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1453 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; DEVELOPMENTAL STAGE: Lymphoid cDNA Library
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; IMMEDIATE SOURCE:
; LIBRARY: Murine Lymphoid
; CLONE: WGA-Resistant Chop Clones
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 206..1453
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..205
US-08-834-108-1
Alignment Scores:
Pred. No.: 2,85e-183 Length: 1453
Score: 1883.50 Matches: 362
Percent Similarity: 94.19% Conservative: 27
Best Local Similarity: 87.65% Mismatches: 19
Query Match: 37.09% Indels: 5
DB: 2 Gaps: 4
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US-10-026-021-2 (1-970) x US-08-834-108-1 (1-1453)
Qy 1 MetAlaThrCysIleGlyGluLysValGlyAspPheLysValGlyAsnLeuLeuGlyLys 20
Db 206 ATGCGCGGTGCATCGGGGAGGATCGAGCACTTTAAGGTTGGAAATCTACTCGGTAAA 265
Qy 21 GlySerPheAlaGlyValTyArgAlaGluSerIleHisThrGlyLeuGluValAlaIle 40
Db 266 GGATCATTTGCTGGTGTCTACAGAGCTGAGTCCATACACACTGGTTTGGAAAGTTGCAATC 325
Qy 41 LysMetIleAaspLysLysAlaMetTyThrLysAlaGlyMetValGlnArgValGlnAsnGlu 60
Db 326 AAAATGTAGATAAGAAAGCCATGTACAACTCGAATGGTACAGAGAGTCCAAAATGAG 385
Qy 61 ValLysIleHisCysGlnLeuLysHisProSerIleLeuGluLeuTyAsnTyPheGlu 80
Db 386 GTGAAATATACATTGCCAGTTGAAACACCCCTCTGCTTGGAGCTCTATAATTACTTTGAA 445
Qy 81 AspSerAsnTyThrValTyLeuValLeuGluMetCysHisAsnGlyGluMetAsnArgTy 100
Db 446 GATAACAAATTTATGCTACCTGGTATTGGAATGTGCCACAATGGAGAAATGAACAGATAT 505
Qy 101 LeuLysAsnArgValLysProPheSerGluAsnGluAlaArgHisPheMetHisGlnIle 120
Db 506 CTGAAGAACAGAAATGAAGCCCTTCTCAGAAAGGAGGAGTAGGCACTTCATGCACCAAT 565
Qy 121 IleThrGlyMetLeuTyThrLeuHisSerHisGlyIleLeuHisArgAspLeuThrLeuSer 140
Db 566 ATCACAGGAATGTTATATCTTCAATTCATGGCATATTTGCCACCGGACCTCACACTCTCT 625
Qy 141 AsnLeuLeuLeuThrArgAsnMetAsnIleLysIleAlaAaspPheGlyLeuAlaThrGln 160
Db 626 AACATCTTACTTCGCGGAATATGAACATAAANAATTTGCTGACTTTGGACTAGCAACGAG 685
Qy 161 LeuLysMetProHisGluLysHisTyThrLeuCysGlyThrProAsnTyThrLeuSerPro 180
Db 686 TTGAATATGCCACATGAAGACACTATACACTCTGTGGGACTCTCTAATATATATTTACCA 745
Qy 181 GluIleAlaThrArgSerAlaHisGlyLeuGluSerAspValTrpSerLeuGlyCysMet 200
Db 746 GAAATTCGAACCTCGAAGTGCAATGGACTTGAATCTGTATATTTGGCTGTATG 805
Qy 201 PheTyThrLeuLeuIleGlyArgProPheAspThrAspThrValLysAsnThrLeu 220
Db 806 TCTTATACGTTACTTATTTGGAAGACCACTTTTGACACTGACACAGTCAAGAACACATGT 865
Qy 221 AsnLysValValLeuAlaAaspTyThrGluMetProSerPheLeuSerIleGluAlaLysAsp 240
Db 866 AACAAAGTAGTCTCGGAGATTATGAATGCGCCTTTTGTGTCAGAGAGCCCGAGAC 925
Qy 241 LeuIleHisGlnLeuLeuArgArgAsnProAlaPheArgLeuSerLeuSerValLeu 260
Db 926 CTTATCCACCACTTACTTCTCGTAGAAACCCCTGCAGATCGGTTAAGTCTGCTCTCTGTTG 985
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QY 261 AspHisProPheMetSerArgHisSerThrLysSerLysSerLysLeuGlyThrValGlu 280  
Db 986 GACCATCTCTTTTATGTCAGCAATCTTCCACCAAGAGTAAAGACCTAGGACTGTAG 1045  
QY 281 AspSerIleAspSerGlyHisAlaThrIleSerThrAlaIleThrAlaSerSerThr 300  
Db 1046 GACTCAATGATAGTGGGATCTACCTTCCACCAATTTACAGCCCTCTTCTGGTACC 1105  
QY 301 SerIleSerGlySerLeuPheAspLysArgArgLeuLeuIleGlyClnProLeuProAsn 320  
Db 1106 AGTTTGGAGTGGCAGCTACTTGCAC---AGAAGACTTTTGGTTGGTCAACCACTTCCAAAT 1162  
QY 321 LysMetThrValPheProLysAsnLysSerThrAspPheSerSerSerGlyAspGly 340  
Db 1163 AAAATTACTGTATTTTCAAAAAAATAAATTCAGTGACTTT---TCTTCAGGAGATGGA 1219  
QY 341 AsnSerPheTyThrGlnTrpGlyAsn-----GlnGluThrSerAsnSerGlyArgGly 358  
Db 1220 AGTATTTTGTACTCAATGGGGAATCCAGAACAGAGAGCTAATAGTAGGGGAGCGGG 1279  
QY 359 ArgValIleGlnAspAlaGluArgProHisSerArgTyThrLeuArgAlaTySer 378  
Db 1280 AGAGTGATGAAGATGCAGAGAGAGGCGCATTTCTCGATACCTGGCAGAGCTCATTC 1339  
QY 379 SerAspArgSerGlyThrSerAsnSerGlnSerGlnAlaLysThrTyThrMetGluArg 398  
Db 1340 TCTGATAGACGAGCCCTCTTAAT---CAGTCTCGAGCAAAACATACCTCAGTAGAGCT 1396  
QY 399 CysHisSerAlaGluMetLeuSerValSerLysArgSer 411  
Db 1397 TGCTACTCAGTAGAAATGCTTTCAAGCCTAGAATCA 1435

## RESULT 8

US-09-016-434-1147  
; Sequence 1147, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016.434  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0002 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1147:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2169 base pairs  
; TYPE: nucleic acid

; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g1488262  
US-09-016-434-1147

## Alignment Scores:

Pred. No.: 5,77e-50 Length: 2169  
Score: 590.50 Matches: 115  
Percent Similarity: 57.33% Conservative: 61  
Best Local Similarity: 37.46% Mismatches: 106  
Query Match: 11.63% Indels: 25  
DB: 4 Gaps: 4  
US-10-026-021-2 (1-970) x US-09-016-434-1147 (1-2169)

QY 15 GlyAsnLeuLeuGlyLysGlySerPheAlaGlyValTyArgAlaGluSerIleHisThr 34  
Db 112 GCGCGCTTTGTTGGGCAAGGGGGCTTCGCCCGCTGTCTACGAGGCCACCTGACACAGAGACT 171  
QY 35 GlyLeuGluValAlaIleLysMetIleAspLysLysAlaMetTyThrLysAlaGlyMetVal 54  
Db 172 GCGAGCGCTACGCTGTCAAAGTCAATCCGAGAGCCGCGTCCGCAAGCCGATCAGCGC 231  
QY 55 GlnArgValGlnAsnGluValLysIleHisCysGlnLeuLysHisProSerIleLeuGlu 74  
Db 232 GAGAAGATCTTAATGAGATTGAGCTGCACCGAGAGCTGCAGACCGCCACATCTGCGCT 291  
QY 75 LeuTyAsnTyThrPheGluAspSerAsnTyThrValTyThrLeuValLeuGluMetCysHisAsn 94  
Db 292 TTTTCGCACCACTTTTGGAGCGCTGCACCACTTACATTTCTTGGAGCTCTGCAGCCGA 351  
QY 95 GlyGluMetAsnArgTyThrLeuLysAsnArgValLysProPheSerGluAsnGluAlaArg 114  
Db 352 AAGTCCCTGGCCCATCTCGAAGCCCGG---CACACCCTGTGTGAGCCAGAGTGGCGC 408  
QY 115 HisPheMetHisGlnIleIleThrGlyMetLeuTyThrGlyHisSerHisGlyIleLeuHis 134  
Db 409 TACTACCTGGCGGAGATCTCTTCTGGCTCAAGTACTTGTGCACCGCGCGGATCTTGCAC 468  
QY 135 ArgAspLeuThrLeuSerAsnLeuLeuLeuThrArgAsnMetAsnIleLysIleAlaAsp 154  
Db 469 CGGACCTCAAGTTGGGAAATTTTTCATCTACTGAGAACATGGAACATGAAGTGGGGAT 528  
QY 155 PheGlyLeuAlaThrGlnLysMetProHisGlyLysHisTyThrLeuCysGlyThr 174  
Db 529 TTTGGCTGGCAGCCCGGTTGGAGCCTCCGAGAGAGAGAGAACCATCTGTGGCACC 588  
QY 175 ProAsnTyThrIleSerProGluIleAlaThrArgSerAlaHisGlyLeuGluSerAspVal 194  
Db 589 CCCAACTATGTGGCTCCAGAGTGTCTGTGAGACAGGCGCCACGCGCTGAGAGCGATGTA 648  
QY 195 TrpSerLeuGlyCysMetPheTyThrLeuLeuIleGlyArgProProPheAspThrAsp 214  
Db 649 TGGTCACTGGGCTGTGTCTATACAGCTGTCTCTCGGGAGCCCTCTCCCTTTGAGACGGCT 708  
QY 215 ThrValLysAsnThrLeuAsnLysValValLeuAlaAspTyThrGluMetProSerPheLeu 234  
Db 709 GACCTGAAGGAGAGCTACCGCTGTCAAGCAGGTTCATACGCTGCTCCCTGCCGCTC 768  
QY 235 SerIleGluAlaLysAspLeuIleHisGlnLeuArgArgAsnProAlaAspArgLeu 254  
Db 769 TCACCTGCTGCCCGGAGCTCTCTGGCGCCATCTTGGGGCTCACCCCGAGACCGCCCC 828  
QY 255 SerLeuSerSerValLeuAspHisProPheMetSerArgAsnSerSerThrLysSerLys 274  
Db 829 TCTATTGACAGATCTCTGGCGCATGACTTCTTTACCAAG----- 867  
QY 275 AspLeuGlyThrValGluAspSerIleAspSerGlyHisAlaThrIleSerThrAlaIle 294  
Db 868 -----GGCTACACCCCGATCGACTC-----CCTATCAGCAGCTGCGCTG 906

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QY 295 ThrAlaSerSerSerThr-----SerIleSerGly 304
|||
Db 907 ACAGTCCCGACCTGACACCCCAACCCAGCTAGAGTCTGTTGGCAAAAGTTACCAAG 966
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QY 305 SerLeuPheAspLysArgArg 311
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Db 967 ACCTCTTTGGCAGAAAGAAG 987
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RESULT 9
US-08-878-989-8
; Sequence 8, Application US/08878989
; Patent No. 5885803
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/878,989
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2770 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HUVENOB01
; CLONE: 39043
US-08-878-989-8

Alignment Scores:
Pred. No.: 1.09e-46 Length: 2770
Score: 560.50 Matches: 163
Percent Similarity: 44.03% Conservativity: 73
Best Local Similarity: 30.41% Mismatches: 200
Query Match: 11.04% Indels: 101
DB: 2 Gaps: 18

US-10-026-021-2 (1-970) x US-08-878-989-8 (1-2770)

QY 15 GlyAsnLeuLeuGlyLysGlySerPheAlaGlyValTyrArgAlaGluSerIleHisThr 34
|||
Db 15 GlyAsnLeuLeuGlyLysGlySerPheAlaGlyValTyrArgAlaGluSerIleHisThr 34
|||
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353 GGCAAGTGTGGGAAAGGGTGGCTTTGCCAAAATGTTACGAGATGACAGATTTGACAAAT 412

35 GlyLeuGluValAlaIleLysMetIleAspLysLysAlaMetTyrLysAlaGlyMetVal 54

413 AACAAAGTCTACGCCGCGCAAAATTTATTCCTCACAGCAGAGTAGCTAAACCTCATCAAGG 472

55 GlnArgValGlnAsnGluValLysIleHisCysGlnLeuLysHisProSerIleLeuGlu 74

473 GAAAGATTTGACAAAGAAATAGAGCTTCACAGAATTTCTCATCATAGCATTAGTGCAG 532

75 LeuTyrAsnTyrPheGluAspSerAsnTyrValTyrLeuValLeuGluMetCysHisasn 94

533 TTTTACCACACTCTTCGAGGACAAAGAAACATTTACATTTCTCTTGGATATCTGCAGTAGA 592

95 GlyGluMetAsnArgTyrLeuLysAsnArgValLysProPheSerGluAsnGluAlaArg 114

593 AGGTCAATGGCTCATATTTTGAAGCAAGA--AAGGTGTTGACAGAGCCAGAAAGTTGGA 649

115 HisPheMetHisGlnIleIleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHis 134

650 TACTACCTCAGGCAGATTGCTCTGACTGAAATACCTTCATGAACCAAGAAATCTTGCAC 709

135 ArgAspLeuThrLeuSerAsnLeuLeuThrArgAsnMetAsnIleLysIleAlaasp 154

710 AGAGATCTCAAACTAGGGAACCTTTTATTATGAAGCCATGGAACATAAAGTTGGGGAC 769

155 PheGlyLeuAlaThrGlnLeuLysMetProHisGlyLysHisTyrThrLeuCysGlyThr 174

770 TTCGCTCTGGCAGCCAGCTAGAACCTTGGAAACACAGAGGAGACATATGTTGTACC 829

175 ProAsnTyrIleSerProGluIleAlaThrArgSerAlaHisGlyLeuGluSerAspVal 194

830 CCAAAATTATCT 889

195 TrpSerLeuGlyCysMetPheTyrThrLeuLeuIleGlyArgProPheAspThrAsp 214

890 TGGCCCTCTGGCTGTGTAAATGTATACATGTTACTAGGAGGCCCCCAATTTGAAACTACA 949

215 ThrValLysAsnThrLeuAsnLysValValLeuAlaAspTyrGluMetProSerPheLeu 234

950 AATCTCAAGAAACTTATAGTGTGCTAAGGGAAGCAAGGTATACATGCGCTCTCATTTG 1009

235 SerIleGluAlaLysAspLeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeu 254

1010 CTGGCTCTCTGCCAAGCAGCTTAATTTGCTAGTAGTGTGTCCAAACCCAGAGAGTGTGCC 1069

255 SerLeuSerValLeuAspHisProPheMetSerArgAsnSerSerThrLysSerLys 274

1070 AGTTTGGATGACATCTTCGACATGACTTTTCTTTTGGCAG----- 1108

275 AspLeuGlyThrValGluAspSerIleAspSerGlyHisAlaThrIleSerThrAlaIle 294

1109 -----GGCTTCACTCCGACAGACTG----- 1129

295 ThrAlaSerSerSerThrSerIleSerGlySerLeuPheAspLysArgArgLeuLeu 314

1130 -----TCTTCTAGCTGTTGTATACAGTTCAGAT-----TTCCACTTA 1168

315 GlyGlnProLeuProAsnLysMetThrValPheProLysAsnLysSerSerThrAspPhe 334

1169 TCAAGCCCGAGCTAAGAAAT-----TCTTTTAAAGAAAGCAGCTGCTGCTCTTTT 1216

335 SerSerSerGlyAspGlyAsnSerPheTyrThrGlnTrpGlyAsnGlnGluThrSerAsn 354

1217 GGTGCAAAAAGACAAAGCAAGATATATT-----GACACACATAAT 1258

355 SerGlyArgGlyArgValIleGlnAspAlaGluGluArgProHisSerArgTyrLeuArg 374

1259 -----AGAGTGTCTTAAAGAAAGATGAAGCATCTCAAGCTTTAGCAT----- 1300

375 ArgAlaTyrSerSerAspArgSerGlyThrSerAsnSerGlnSerGlnAlaLysThrTyr 394

1301 -----GATTTGAAAAGACTTCAATACTCAAGCAACCCAGCAACACACAGG 1345

QY 395 ThrMetGluArgCysHisSerAlaGluMetLeuSerValSerIysSerGlyGly 414  
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Db 1346 ACAGATGAGGAGCTCCAGCCACCT-----ACCACACAGATGTCAGAGTCTGGAACACCC 1399  
QY 415 GluAsnGluGluArgTyrSerProThrAspAsnAlaAsnIlePheAsnPhePheLys 434  
|||  
Db 1400 GCAGTAGAACAACAGCAGAGATGGGATGCTATTCCGATGATAGTCAGAGGACTCTT 1459  
QY 435 GluLysThrSerSerSerGlySerPheGluArgProAspAsnAsnGln-----451  
|||  
Db 1460 GCAGCTGTAGCAGCAGCAGTGAATGCTTGA-----GACAGTACCATGGGAAGTGT 1513  
QY 452 -----AlaLeuSerAsnHisLeuCysProGlyLys 461  
|||  
Db 1514 GCAGACACAGTGCAGAGGTTCTTCGGGATGCTCGAAGAAC-----1555  
QY 462 ThrProPheProPheAlaAsp-----ProThrProGlnThrCluThrValGlnGlnTTP 479  
|||  
Db 1556 -----ATCGCGAAGCTGATTGCAATCCCAAGACGCTGAGCACATCATTTTCAGTGG 1609  
QY 480 -----PheGlyAsnLeuGlnIleAsnAla 487  
|||  
Db 1610 GTCACCAATGGTGTGATTACTCTAACAATATGGCTTTGGG---TACAGCTCTCAGAC 1666  
QY 488 HisLeuArgLysThrThrGluTyrAspSerIleSerProAsnArgAspPheGlnGlyHis 507  
|||  
Db 1667 CACAC-CGTGG-----TGCTCTTTTCAACAATGGTCTCACAT 1704  
QY 508 -----ProAspLeuGlnLysAspThrSer-----LysAsnAlaTTP 519  
|||  
Db 1705 GAGCTCTCTCCAGACACAAAAAACAGCTCACTATTACGAGAGCTTGG 1752

## RESULT 10

US-09-272-796-8  
; Sequence 8, Application US/09272796  
; Patent No. 6207148  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl G.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/272,796  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/878,989  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J J  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0321 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2770 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: HUVEBO01  
; CLONE: 39043  
; US-09-272-796-8  
  
Alignment Scores:  
Pred. No.: 1.09e-46 Length: 2770  
Score: 560.50 Matches: 163  
Percent Similarity: 44.03% Conservative: 73  
Best Local Similarity: 30.41% Mismatches: 200  
Query Match: 11.04% Indels: 101  
DB: 3 Gaps: 18

US-10-026-021-2 (1-970) x US-09-272-796-8 (1-2770)

QY 15 GlyAsnLeuLeuGlyLysGlySerPheAlaGlyValTyrArgAlaGluSerIleHisThr 34  
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Db 353 GGCAGAGTCTCGGGAAGGGTGGCTTTCGCAAAATGTTACGAGATGACAGATTGCAAAAT 412  
QY 35 GlyLeuGluValAlaIleLysMetIleAspLysAlaMetTyrLysAlaGlyMetVal 54  
|||  
Db 413 AACAAAGTCTACGCGCAAAATATTCTCTCAGCAGAGTAGCTAAACCTCATCAAGG 472  
QY 55 GlnArgValGlnAsnGluValLysIleHisCysGlnLeuLysHisProSerIleLeuGlu 74  
|||  
Db 473 GAAAGATTGCAAGAAATAGAGCTTCACAGAAATTTCTCATCAATAGCATGTAGTGCAG 532  
QY 75 LeuTyrAsnTyrPheGluAspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsn 94  
|||  
Db 533 TTTTACCACCTACTCTCGAGCAAAAGAAACATTATCTCTTGGAAATAGCTGCAGTAGA 592  
QY 95 GlyGluMetAsnArgTyrLeuLysAsnArgValLysProPheSerGluAsnGluAlaArg 114  
|||  
Db 593 AGGTCAATGGCTCATATTTTGAAGCAAGA---AAGTGTTCAGAGCCAGCAAGTTCGA 649  
QY 115 HisPheMetHisGlnIleIleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHis 134  
|||  
Db 650 TACTACCTCAGGCAGATTGTGCTCGACTGAAATACCTTCATGAACAAGAAATCTTGCAC 709  
QY 135 ArgAspLeuThrLeuSerAsnLeuLeuThrArgAsnMetAsnIleLysIleAlaAsp 154  
|||  
Db 710 AGAGATCTCAAACTAGGGAACCTTTTATTATGAAGCCATGGAACCTAAAGTTGGGGAC 769  
QY 155 PheGlyLeuAlaThrGlnLysMetProHisGluLysHisTyrThrLeuCysGlyThr 174  
|||  
Db 770 TTCGGTCTGGCAGCCAGCTAGAACCTTTTGAACACAGAGAGAGACGATATGTGTGACC 829  
QY 175 ProAsnTyrIleSerProGluIleAlaThrArgSerAlaHisGlyLeuGluSerAspVal 194  
|||  
Db 830 CCAAAATTATCTCTCTCTGAGTCTCAACAAACAGGACATGGCTGTGAATCAGACATT 889  
QY 195 TrpSerLeuGlyCysMetPheTyrThrLeuLeuIleGlyArgProPheAspThrAsp 214  
|||  
Db 890 TGGGCCCTGGGCTGTGTAATGATATCAATGTTACTAGGAGGAGGCCCCCATTTGAAACTACA 949  
QY 215 ThrValLysAsnThrLeuAsnLysValValLeuAlaAspTyrGluMetProSerPheLeu 234  
|||  
Db 950 AATCTCAAGAAACATTATAGGTGTCATAGGGAAGCAAGGTATACATATGCCGCTCATTTG 1009  
QY 235 SerIleGluAlaLysAspLeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeu 254  
|||  
Db 1010 CTGGCTCTGCGCAAGCACTTAATTCCTAGTAGTGTGTCACAAAACCCAGAGATGCTCCC 1069  
QY 255 SerLeuSerSerValLeuAspHisProPheMetSerArgAsnSerSerThrLysSerLys 274  
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Db 1070 AGTTTGGATGACATCATTCGACATGCTTTTTTTTTCAG----- 1108
Qy 275 AspLeuGlyThrValGluAspSerIleAspSerGlyHisAlaThrIleSerThrAlaIle 294
Db 1109 -----GGCTTCACCTCCGACAGACTG----- 1129
Qy 295 ThrAlaSerSerThrSerIleSerGlySerLeuPheAspLysArgLeuLeuIle 314
Db 1130 -----TCCTCTAGCTGTGTCTACAGTTCAGAT-----TTCACACTA 1168
Qy 315 GlyGlnProLeuProAsnLysMetThrValPheProLysAsnLysSerSerThrAspPhe 334
Db 1169 TCAAGCCCACTAAGAAAT-----TTCCTTAAGAAAGCAGCTGCTGCTCTTTT 1216
Qy 335 SerSerSerGlyAspGlyAsnSerPheThrGlnTrpGlyAsnGlnGluThrSerAsn 354
Db 1217 GGTGCAAAAGACAAAGCAAGATATAT-----GACACACATAAT 1258
Qy 355 SerGlyArgGlyArgValIleGlnAspAlaGluArgProHisSerArgTrpLeuArg 374
Db 1259 -----AGATGCTTAAGAGATGAAGACATCTCAAGCTTAGGCAT----- 1300
Qy 375 ArgAlaTySerSerAspArgSerGlyThrSerAsnSerGlnSerGlnAlaLysThrTy 394
Db 1301 -----GATTTGAAAAGACTTCAATAACTCACAACCCAGCAACACACAGG 1345
Qy 395 ThrMetGluArgCysHisSerAlaGluMetLeuSerValSerLysArgSerGlyGly 414
Db 1346 ACAGATGAGGAGCTCCAGCACT-----ACCACCACAGTTGCCAGGTCTGGAACACCC 1399
Qy 415 GluAsnGluGluArgTySerProThrAspAsnAlaAsnIlePheAsnPhePheLys 434
Db 1400 GCAGTAGAAAACACAGCAGAGATGGGGATGCTATTCGGATGATAGTCAGAGGACTT 1459
Qy 435 GluLysThrSerSerSerGlySerPheGluArgProAspAsnAsnGln----- 451
Db 1460 GCAGCTGTAGCAGCAGCAGTGAATGCTTTGAA-----GACAGTACCAGGAAGTGT 1513
Qy 452 -----AlaLeuSerAsnHisLeuCysProGlyLys 461
Db 1514 GCAGACACAGTGCGAAGGTTCTTCGGGATGCTCTGGAAC----- 1555
Qy 462 ThrProPheProPheAlaAsp-----ProThrProGlnThrGluThrValGlnGlnTrp 479
Db 1556 -----ATCCGGAAGCTGATTCATTCCTCCAAAGACAGCTCAGACATCATTCAGTGG 1609
Qy 480 -----PheGlyAsnLeuGlnIleAsnAla 487
Db 1610 GTCAACCAATGGTTGATTACTCTAACAAATATGGCTTTTGG--TACCAGCTCTCAGAC 1666
Qy 488 HisLeuArgLysThrThrGluTyraSpSerIleSerProAsnArgAspPheGlnGlyHis 507
Db 1667 CACAC-CGTGCG-----TGTCTCTTTCAACAATGGTGTCTCAGAT 1704
Qy 508 -----ProAspLeuGlnLysAspThrSer-----LysAsnAlaTrp 519
Db 1705 GAGCTCTCTCCAGACAAAAAACAGCTCACTATTACGAGAGCTTGG 1752
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## RESULT 11

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US-09-136-282-3
; Sequence 3, Application US/09136282
; Patent No. 6063609
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, KAREN
; APPLICANT: JACKSON, JEFFREY
; APPLICANT: HANSBURY, MICHAEL
; APPLICANT: NERURKAR, SANDHYA
; APPLICANT: ROSKAY, AMY
; APPLICANT: BOUZYK, MARK
; TITLE OF INVENTION: HUMAN SERUM INDUCIBLE KINASE (SNK)
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
```

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; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,282
; FILING DATE: 20-AUG-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/056,112
; FILING DATE: 20-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70231
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-136-282-3
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## Alignment Scores:

Pred. No.:	1,1e-46	Length:	2789
Score:	560.50	Matches:	163
Percent Similarity:	44.03%	Conservative:	73
Best Local Similarity:	30.41%	Mismatches:	200
Query Match:	11.04%	Indels:	101
DB:	3	Gaps:	18

US-10-026-021-2 (1-970) x US-09-136-282-3 (1-2789)

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Qy 15 GlyAsnLeuLeuGlyLysGlySerPheAlaGlyValTyArgAlaGluSerIleHisThr 34
Db 370 GGCAAAGTCTGCGGAAAGGGTGGCTTTGC AAAATGTTACGAGATGACAGATTTGACAAAT 429
Qy 35 GlyLeuGluValAlaIleLysMetIleAspLysLysAlaMetTyLysAlaGlyMetVal 54
Db 430 AACAAAGTCTACGCGCGCAAAAATTTATTCCTCACAGCAGAGTAGGTAAACCTCATCAAAGG 489
Qy 55 GlnArgValGlnAsnGluValLysIleHisCysGlnLeuLysHisProSerIleLeuGlu 74
Db 490 GAAAGATTGACAAAGAAATAGAGCTTCACAGAATTCCTCATCATAGCATGTAGTGCGAG 549
Qy 75 LeuTyraSerTyPheGluAspSerAsnTyValTyLeuValLeuGluMetCysHisAsn 94
Db 550 TTTTACCACCTACTTCGAGGACAAAAGAAAATTTACATTTCTCTTGGAAATCTTGCAGTAGA 609
Qy 95 GlyGluMetAsnArgTyTrpLeuLysAsnArgValLysProPheSerGluAsnGluAlaArg 114
Db 610 AGGTCAATGGCTCATATTTTGAAGCAAGA---AAGGTGTTGACAGACCCAGAGTTTGA 666
Qy 115 HisPheMetHisGlnIleIleThrGlyMetLeuTyLysHisSerHisGlyIleLeuHis 134
Db 667 TACTACCTCAGCAGATTGTCTGGAAGTAAATACCTTCATGAACAAGAAATCTTGAC 726
Qy 135 ArgAspLeuThrLeuSerAsnLeuLeuThrArgAsnMetAsnIleLysIleAlaAsp 154
Db 727 AGAGATCTCAAACTAGGGAACCTTTTATTATTAAGAACCACTGGAACATAAAAGTTGGGAC 786
Qy 155 PheGlyLeuAlaThrGlnLeuLysMetProHisGluLysHisTyThrThrCysGlyThr 174
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Db 490 GAAAGATTGACAAAGAAATAGAGCTTCACAGAAATTCATCATTAAGCATGTAGTCGAG 549  
Qy 75 LeuTyrAsnTyrPheGluAspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsn 94  
Db 550 TTTTACCACACTCTCGAGGACAAAGAAACATTTACATTCCTCTGGAATAGTCGAGTAGA 609  
Qy 95 GlyGluMetAsnArgTyrLeuLysAsnArgValLysProPheSerGluAsnGluAlaArg 114  
Db 610 AG-GCAATGGCTCATATTTGAAAGCAAGA---AAGGTGTTTGACAGAGCCAGAAAGTTGGA 665  
Qy 115 HisPheMetHisGlnIleThrGlyMetLeuTyrLeuHisSerHisGlyLeuHis 134  
Db 666 TACTACCTCAGCAGCATGTGCTGAGCTGAATACCTTCATGAAACAAGAAATCTTTGCAC 725  
Qy 135 ArgAspLeuThrLeuSerAsnLeuLeuThrArgAsnMetAsnIleLysIleAlaAsp 154  
Db 726 AGAGATCTCAAACTAGGGAACCTTTTATTATGAAGCCATGAAGTAAGTTGGGAC 785  
Qy 155 PheGlyLeuAlaThrGlnLeuLysMetProHisGluLysHisTyrThrLeuCysGlyThr 174  
Db 786 TTCGCTCTGGCAGCCAGGCTAGAACCTTGGAACACAGAGGAGAACGATATGTGTACC 845  
Qy 175 ProAsnTyrIleSerProGluIleAlaThrArgSerAlaHisGlyLeuGluSerAspVal 194  
Db 846 CCAAAATTAATCTCTCTCCTGAAGTCTCAACAAACAGGACATGGCTGTGAATCAGACAT 905  
Qy 195 TrpSerLeuGlyCysMetPheTyrThrLeuLeuIleGlyArgProPheAspThrAsp 214  
Db 906 TGGGCGCTGGCTGTGTATGATATACATGTTACTAGGAGGCCCCCAATTTGAAACTACA 965  
Qy 215 ThrValLysAsnThrLeuAsnLysValValLeuAlaAspTyrGluMetProSerPheLeu 234  
Db 966 AATCTCAAAAGAACTTATAGGTGCATAGGGAAGCAAGTATACAAATGCCGCTCATTTG 1025  
Qy 235 SerIleGluAlaLysAspLeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeu 254  
Db 1026 CTGGCTCTGCCAACGACCTTAATCTCTAGTATGTTGTCCAAACCCAGAGGATAGGCT 1085  
Qy 255 SerLeuSerValLeuAspHisProPheMetSerArgAsnSerSerThrLysSerLys 274  
Db 1086 AGTTTGGATGACATCATTCGACATGACATTTTTTTTGGCAG----- 1124  
Qy 275 AspLeuGlyThrValGluAspSerIleAspSerGlyHisAlaThrIleSerThrAlaIle 294  
Db 1125 -----GGCTTCACTCCGACAGACTG----- 1145  
Qy 295 ThrAlaSerSerSerThrSerIleSerGlySerLeuPheAspLysArgArgLeuLeuIle 314  
Db 1146 -----TCTTCTAGCTGTTGTGCATACATGTTCCAGAT-----TTCACCTTA 1184  
Qy 315 GlyGlnProLeuProAsnLysMetThrValPheProLysAsnLysSerSerThrAspPhe 334  
Db 1185 TCAAGCCCGACTAAGAAT-----TTCTTTAAGAAAGCAGCTGCTGCTCTTTT 1232  
Qy 335 SerSerSerGlyAspGlyAsnSerPheTyrThrGlnTrpGlyAsnGlnGluThrSerAsn 354  
Db 1233 GGTGCAAAAGACAAAGCAAGATATATT-----GACACATATAT 1274  
Qy 355 SerGlyArgGlyArgValIleGlnAspAlaGluArgProHisSerArgTyrLeuArg 374  
Db 1275 -----AGAGTGCTAAAGAAAGTGAAGACATCTACAAAGCTTAGGCAT----- 1316  
Qy 375 ArgAlaTyrSerSerAspArgSerGlyThrSerAsnSerGlnSerGlnAlaLysThrTyr 394  
Db 1317 -----GATTTGAAAAGACTTCAATACTCAGCAACCCAGCAACACAGG 1361  
Qy 395 ThrMetGluArgCysHisSerAlaGluMetLeuSerValSerLysArgSerGlyGlyGly 414  
Db 1362 ACAGATGAGGAGCTCCAGCCACCT-----ACCACACAGTGTCCAGGCTCTGGAACACCC 1415  
Qy 415 GluAsnGluArgTyrSerProThrAspAsnAsnAlaAsnIlePheAsnPhePheLys 434

Db 1416 GCAGTAGAAAAACAACAGCAGCAGATGGGGATGCTATTTCGGATGATAGTCAGAGGGACTCTT 1475  
Qy 435 GluLysThrSerSerSerGlySerPheGluArgProAspAsnAsnGln----- 451  
Db 1476 GGCAGCTGTACGACGACGAGTGAATGCCTTGA-----GACAGTACCATGGGAAGTGT 1529  
Qy 452 -----AlaLeuSerAsnHisLeuCysProGlyLys 461  
Db 1530 GCAGACACAGTGGCAAGGGTTCTTGGGGATGTCTGGAAGAAC----- 1571  
Qy 462 ThrProPheProPheAlaAsp-----ProThrProGlnThrGluThrValGlnGlnTrp 479  
Db 1572 -----ATGCCGGAAGCTGATTCATTCCTCCAAAGCAGCTGAGCAGCATCATTTCACTGG 1625  
Qy 480 -----PheGlyAsnLeuGlnIleAsnAla 487  
Db 1626 GTCACCAAAATGGTGTGATTACTCTAAACAAATATGCTTTTGGG---TACCAGCTCTCAGAC 1682  
Qy 488 HisLeuArgLysThrThrGluTyrAspSerIleSerProAsnArgAspPheGlnGlyHis 507  
Db 1683 CACAC-CGTGCG-----TGTCCTTTTCAACAATGGTGTCTCACAT 1720  
Qy 508 -----ProAspLeuGlnLysAspThrSer-----LysAsnAlaTrp 519  
Db 1721 GAGCTCTCTTCCAGACAAAAAAGATTCATATTACGACAGCTTGG 1768

## RESULT 14

US-09-505-744-1  
; Sequence 1, Application US/09505744  
; Patent No. 6245544  
; GENERAL INFORMATION:  
; APPLICANT: Karen M. Anderson  
; APPLICANT: Mark M. Bouzyk  
; APPLICANT: Michael J. Hanebury  
; APPLICANT: Jeffrey R. Jackson  
; APPLICANT: Sandhya S. Nerurkar  
; APPLICANT: Amy K. Koshak  
; TITLE OF INVENTION: HUMAN SERUM INDUCIBLE KINASE (SNK)  
; FILE REFERENCE: GH-70231-D1  
; CURRENT APPLICATION NUMBER: US/09/505,744  
; EARLIER FILING DATE: 2000-02-16  
; EARLIER APPLICATION NUMBER: 09/136,282  
; EARLIER FILING DATE: 1998-08-20  
; EARLIER APPLICATION NUMBER: 60/056,112  
; EARLIER FILING DATE: 1997-08-20  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 2783  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (2720) (2721)  
US-09-505-744-1

Alignment Scores:  
Pred. No.: 2,01e-44 Length: 2783  
Score: 538.50 Matches: 163  
Percent Similarity: 44.03% Conservative: 73  
Best Local Similarity: 30.41% Mismatches: 200  
Query Match: 10.60% Indels: 102  
DB: 3 Gaps: 18

US-10-026-021-2 (1-970) x US-09-505-744-1 (1-2783)

Qy 15 GlyAsnLeuLeuGlyLysGlySerPheAlaGlyValTyrArgAlaGluSerIleHisThr 34  
Db 370 GGCAAGTGTGGGAGGGTGGCTTTGCCAAAATGTTACGAGATGACAGATTTGCAAAAT 429  
Qy 35 GlyLeuGluValAlaIleLysMetIleAspLysLysAlaMetTyrLysAlaGlyMetVal 54  
Db 430 AACAAAGTCTACGCCGCAAAAATTTATTCTCTCACAGCAGAGTAGCTAAACCTCATCAAGG 489

QY 55 GlnArgValGlnAsnGluValLysIleHisCysGlnLeuLysHisProSerIleLeuGlu 74  
Db 490 GAAAGATTGACAAAGAAATAGAGCTTCACAGAAATTCATCATCAAGCATGTAGTCGAC 549  
QY 75 LeuTyrAsnTyrPheGluAspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsn 94  
Db 550 TTTTACCCTACTTCGAGGACAAAGAAACATTTACATCTCTTGGATATCTGACAGTAGA 609  
QY 95 GlyGluMetAsnArgTyrLeuLysAsnArgValLysProPheSerGluAsnGluAlaArg 114  
Db 610 AG-GCAATGGCTCATATTTGAAAGCAAGA--AAGGTGTTGACAGAGCCAGAACTTCCA 665  
QY 115 HisPheMetHisGlnIleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHis 134  
Db 666 TACTACCTCAGGACGATGTGCTGACCTGAATACCTTCATGAACAAGAAATCTTGCAC 725  
QY 135 ArgAspLeuThrLeuSerAsnLeuLeuThrArgAsnMetAsnIleLysIleAlaAsp 154  
Db 726 AGAGATCTCAAACTAGGGAACCTTTTATTATGAGCCATGGAACCTAAAGTTGGGAC 785  
QY 155 PheGlyLeuAlaThrGlnLeuLysMetProHisGluLysHisTyrThrLeuCysGlyThr 174  
Db 786 TTCGGTCTGGCAGCCAGGTAGAACCCCTTGGAAACACAGAGGAGACGATATGTGTACC 845  
QY 175 ProAsnTyrIleSerProGluIleAlaThrArgSerAlaHisGlyLeuGluSerAspVal 194  
Db 846 CAAATATTCT 905  
QY 195 TrpSerLeuGlyCysMetPheTyrThrLeuLeuIleGlyArgProPheAspThrAsp 214  
Db 906 TGGGCCCTGGCTGTGTATGATATACATGTTACTAGGAGGCCCTCAATTTGAACACTACA 965  
QY 215 ThrValLysAsnThrLeuAsnLysValValLeuAlaAspTyrGluMetProSerPheLeu 234  
Db 966 AATCTCAAGAAACTATAGGTGCATAGGGAAGCAAGGTATACAAATGCCGCTCATTTG 1025  
QY 235 SerIleGluAlaLysAspLeuIleHisGlnLeuLeuArgAsnProAlaAspArgLeu 254  
Db 1026 CTGGCTCTGCCAAGCAGCTTAATGCTAGTGTGTCCTCAAAACCCAGAGATAGGCT 1085  
QY 255 SerLeuSerSerValLeuAspHisProPheMetSerArgAsnSerSerThrLysSerLys 274  
Db 1086 AGTTTGGATGACATCATTCGACATGACATTTTTTTTTCAG----- 1124  
QY 275 AspLeuGlyThrValGluAspSerIleAspSerGlyHisAlaThrIleSerThrAlaIle 294  
Db 1125 -----GGCTTCACTCCGACAGACTG----- 1145  
QY 295 ThrAlaSerSerThrSerIleSerGlySerLeuPheAspLysArgArgLeuLeuIle 314  
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QY 315 GlyGlnProLeuProAsnLysMetThrValPheProLysAsnLysSerSerThrAspPhe 334  
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RESULT 15  
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; Sequence 1, Application US/09198122  
; Patent No. 6180380  
; GENERAL INFORMATION:  
; APPLICANT: Streibhardt, Klaus; Rubsamen-Waigmann, Helga;  
; APPLICANT: Holtrich, Uwe  
; TITLE OF INVENTION: CLONING OF A MEMBER OF THE SERINE-  
; TITLE OF INVENTION: THREONINE-KINASE FAMILY  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SPRUNG HORN KRAMER & WOODS  
; STREET: 660 White Plains Road  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10591-5144  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB  
; MEDIUM TYPE: storage  
; COMPUTER: NEC Powermate SX-20  
; OPERATING SYSTEM: DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/198,122  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/601,014  
; FILING DATE: 23-FEB-1996  
; APPLICATION NUMBER: PCT/EP94/02863  
; FILING DATE: 30-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE 4329177  
; FILING DATE: 30-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kurt G. Briscoe  
; REGISTRATION NUMBER: 33,141  
; REFERENCE/DOCKET NUMBER: Bayer 9516-KGB  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (914) 332-1700  
; TELEFAX: (914) 332-1844  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:



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(without alignments)  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	5075	99.9	3937	15	US-10-037-270-280	Sequence 280, App
3	5075	99.9	3937	17	US-10-117-722-280	Sequence 280, App
4	5071	99.9	3721	14	US-10-116-802-108	Sequence 108, App
5	5067	99.8	3092	20	US-10-737-450-89	Sequence 89, Appl
6	5057	99.6	3331	21	US-10-887-553A-750	Sequence 750, App
7	4861	95.7	2836	18	US-10-425-114-2625A	Sequence 2625A, A
8	4777.5	94.1	3924	17	US-10-062-674-1868	Sequence 1868, Ap
9	743	14.6	484	10	US-09-918-995-21560	Sequence 21560, A
10	594	11.7	328	9	US-09-878-178-96	Sequence 96, Appl
11	594	11.7	328	13	US-10-046-335-96	Sequence 96, Appl
12	594	11.7	328	14	US-10-146-502-96	Sequence 96, Appl
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14	590.5	11.6	2169	16	US-10-204-041-15	Sequence 15, Appl
15	590.5	11.6	2169	17	US-10-305-720-1147	Sequence 1147, Ap
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17	590.5	11.6	2169	19	US-10-620-052A-27	Sequence 27, Appl
18	590.5	11.6	2169	21	US-10-781-581-215	Sequence 215, App
19	590.5	11.6	2378	19	US-10-755-889-3	Sequence 3, Appl
20	590.5	11.6	2535	19	US-10-618-941-34	Sequence 34, Appl
21	589.5	11.6	2410	19	US-10-304-116-12	Sequence 12, Appl
22	567.5	11.2	2781	17	US-10-191-803-222	Sequence 222, App
23	567.5	11.2	2781	18	US-10-152-319A-1953	Sequence 1953, Ap
24	567.5	11.2	2781	21	US-10-764-420-538	Sequence 538, App
25	564.5	11.1	2772	21	US-10-764-420-944	Sequence 944, Appl
26	560.5	11.0	2770	10	US-09-769-970-8	Sequence 8, Appl
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33	560.5	11.0	2972	17	US-10-159-563-102	Sequence 102, App
34	560.5	11.0	2972	18	US-10-342-887-1302	Sequence 1302, Ap
35	560.5	11.0	2972	18	US-10-260-708-24	Sequence 24, Appl
36	560.5	11.0	2972	21	US-10-651-237-94	Sequence 94, Appl
37	560.5	11.0	2972	21	US-10-782-413-94	Sequence 94, Appl
38	560.5	11.0	2976	17	US-10-264-049-949	Sequence 949, App
39	560.5	11.0	3024	14	US-10-198-846-11031	Sequence 11031, A
40	559.5	11.0	3960	20	US-10-723-860-7079	Sequence 7079, Ap
41	545.5	10.7	2955	19	US-10-437-963-34025	Sequence 34025, A
42	539.5	10.6	2778	14	US-10-059-585-13	Sequence 13, Appl
43	536	10.6	2137	19	US-10-283-975A-283	Sequence 283, App
44	536	10.6	2137	21	US-10-487-422-88	Sequence 88, Appl
45	536	10.6	2137	21	US-10-487-422-102	Sequence 102, App

ALIGNMENTS

RESULT 1  
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; Sequence 1, Application US/10026021  
; Publication No. US20030027756A1  
; GENERAL INFORMATION:  
; APPLICANT: Hitoshi, Yasumichi  
; APPLICANT: Demo, Susan  
; APPLICANT: Jenkins, Yonchu  
; APPLICANT: Rigel Pharmaceuticals, Inc.  
; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for  
; TITLE OF INVENTION: Treatment of Cancer  
; FILE REFERENCE: 021044-001210US  
; CURRENT APPLICATION NUMBER: US/10/026.021  
; PRIORITY FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: US 60/309,632  
; PRIOR FILING DATE: 2001-08-01

; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1  
 ; LENGTH: 2913  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(2913)  
 ; OTHER INFORMATION: human SAK serine/threonine kinase  
 US-10-026-021-1

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 Percent Similarity: 100.00% Conservativity: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 14 Gaps: 0

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QY 921 AlaGlyValSerSerIleSerTyrThrSerProAsnGlyGlnThrThrArgTyrGlyGlu 940
Db 2761 GCAGGAGTGTCTTCTATCAGTTATACCTCAACAAATGGTCAACAACTAGGTATGAGAA 2820
QY 941 AsnGluLysLeuProAspTyrIleLysGlnLysLeuGlnCysLeuSerSerIleLeuLeu 960
Db 2821 AATGAAAAATTACGACTACATCAACACAGAAATTAACAGTGTCTGTCTTCCATCCTTTTG 2880
QY 961 MetPheSerAsnProThrProAsnPheHis 970
Db 2881 ATGTTTCTTAATCCGACTCCTAATTTTCAT 2910
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RESULT 2

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US-10-037-270-280
; Sequence 280, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Tillinghaast, John
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/10/037, 270
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 09/552, 317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488, 725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt FL_genes Version 1.0
; SEQ ID NO 280
; LENGTH: 3937
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (334) .. (3246)
US-10-037-270-280

Alignment Scores:
Pred. No.: 0 Length: 3937
Score: 5075.00 Matches: 969
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.90% Mismatches: 0
Query Match: 99.94% Indels: 0
DB: 15 Gaps: 0

US-10-026-021-2 (1-970) x US-10-037-270-280 (1-3937)
QY 1 MetAlaThrCysIleGlyGluValIleGluAspPheLysValGlyAsnLeuLeuGlyLys 20
Db 334 ATGGCGACTGTCATCGGGGAGAGATCAGGATTTTAAAGTTGGAATCTGCTTGGTAAA 393
QY 21 GlySerPheAlaGlyValTyrArgAlaGluSerIleHisThrGlyLeuGluValAlaIle 40
Db 394 GGATCATTTGCTGGTGTCTACAGACTGAGTCCATTCACACTGGTTTGGAGTTGCAATC 453
QY 41 LysMetIleAspLysLysAlaMetTyrLysAlaGlyMetValGlnArgValGlnAsnGlu 60
Db 454 AAAATGATAGATAAGAAAGCCATGTACAAAGCAGGAATGGTACAGAGAGTCCAAAATGAG 513
QY 61 ValLysIleHisCysGlnLeuLysHisProSerIleLeuGluLeuTyrAsnTyrPheGlu 80
Db 514 GTGAAAAATACATTTGCCAATTGAAACATCTTCTATCTTTGGAGCTTTATAACTATTTTGA 573
QY 81 AspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsnGlyGluMetAsnArgTyr 100
Db 574 GATAGCAATTATGTATCTGGTATTAGAAATGTGCCAATATGGAGAAATGAACAGGTAT 633
QY 101 LeuLysAsnArgValLysProPheSerGluAsnGluAlaArgHisPheMetHisGlnIle 120
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634 CTAAGAATAGAGTGAACCCCTTCTCAGAAAATGAGCTCGACACTTCATGACCAGATC 693  
121 IleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHisArgAspLeuThrLeuSer 140  
694 ATCACAGGATGTTGATCTTCATCTCATGTTATACACCGGACCTCACACTTCT 753  
141 AsnLeuLeuThrArgAsnMetAsnIleLysIleAlaAspPheGlyLeuAlaThrGln 160  
754 AACCTCCTACTGACTCGTAAATATGAACATCAAGATTGCTGATTTTGGCGTGGCACTCAA 813  
161 LeuLysMetProHisGlyLysHisTyrThrLeuCysGlyThrProAsnTyrIleSerPro 180  
814 CTGAAAATGCCACATGAAAGACATATACATTTATGTGGNACTCTTAACATCACTTCACCA 873  
181 GluIleAlaThrArgSerAlaHisGlyLeuGluSerAspValTyrSerLeuGlyCysMet 200  
874 GAAATGGCCACTCGAAGTCACATGGCCTTGAATCTGATGTTTGGTCCCTGGGCTGTATG 933  
201 PheTyrThrLeuLeuIleGlyArgProPheAspThrAspThrValLysAsnThrLeu 220  
934 TTTTATACATTAATCTATCGGGAGACCCCTTCGACACTGCACAGTCAAGAACACATTA 993  
221 AsnLysValValLeuAlaAspTyrGluMetProSerPheLeuSerIleGluAlaLysAsp 240  
994 AATAAGTAGTATTGGCAGATTATGNAATGCCAATCTTTTGTCAATAGAGGCCAAGGAC 1053  
241 LeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeuSerLeuSerValLeu 260  
1054 CTATTACCAGTTACTTCGTAGNAATCCAGCAGATCGTTTAAAGTCTGCTTTCAGTATTG 1113  
261 AspHisProPheMetSerArgAsnSerSerThrLysSerLysAspLeuGlyThrValGlu 280  
1114 GACCATCTCTTTATGTCGCGAAATCTTCAACAAAAGTAAAGATTTAGGAACTGTGGAA 1173  
281 AspSerIleAspSerGlyHisAlaThrIleSerThrAlaIleThrAlaSerSerThr 300  
1174 GACTCAATTTGATGTGGGATGCCCAATTTCTACTGCDAATTTACAGCTTCTTCCAGTACC 1233  
301 SerIleSerGlySerLeuPheAspLysArgArgLeuLeuIleGlyGlnProLeuProAsn 320  
1234 AGTATAAGTGGTAGTTTATTCACAAAAGAGACATTTTGTGATTTGGTCAGCCACTCCCAAT 1293  
321 LysMetThrValPheProLysAsnLysSerSerThrAspPheSerSerSerGlyAspGly 340  
1294 AAAATGACTGTATTTCCAAAGAAATAAAGTTCAACTGATTTTCTCTTCAGAGATGGA 1353  
341 AsnSerPheTyrThrGlnTyrGlyAsnGlnGluThrSerAsnSerGlyArgGlyArgVal 360  
1354 AACAGTTTTTACTCAGTGGGGAATCAAGAAACCGATTAAGTGGAGGGGAGAGATA 1413  
361 IleGlnAspAlaGluArgProHisSerArgTyrLeuArgArgAlaTyrSerSerAsp 380  
1414 ATTCAAGATGCAGAAAGGCGCACATCTCGATACCTTCGTAGAGCTTATTCCTCGAT 1473  
381 ArgSerGlyThrSerAsnSerGlnSerGlnAlaLysThrTyrThrMetGluArgCysHis 400  
1474 AGATCTGGCAGCTCTTAATAGTCAGTCTCAAGCAAAACATATACAAATGGAACGATGTAC 1533  
401 SerAlaGluMetLeuSerValSerLysArgSerGlyGlyGlyGluAsnGluGluArgTyr 420  
1534 TCAGCAGAAATGCTTTTCAGTGTCCAAAGATCAGGAGGGGTGAAAATGAAAGAGGTAC 1593  
421 SerProThrAspAsnAsnAlaAsnIlePheAsnPheLysGlyLysThrSerSerSer 440  
1594 TCACCCACACAGACAAATGCAACATTTTAACTCTTTAAAGAAAAGACATCCAGTAGT 1653  
441 SerGlySerPheGluArgProAspAsnAsnGlnAlaLeuSerAsnHisLeuCysProGly 460  
1654 TCTGGATCTTTTGAAGAGCTGTATAACAATCAAGCACTCTCCAATCATCTTTGTCCAGGA 1713  
461 LysThrProPheProPheAlaAspProThrProGlnThrGluThrValGlnGlnTyrPhe 480  
1714 AAAACTCTTTTCCATTTGCAGACCCGACACCTCAGACTGMAACCGTACAAACAGTGGTTT 1773

QY GlyAsnLeuGlnIleAsnAlaHisLeuArgLysThrThrGluTyrAspSerIleSerPro 500  
Db GGGAAATCTGCAATAATAATGCTCTATTTAAGAAAACTACTGAATATGACAGCATCAGCCCA 1833  
QY AsnArgAspPheGlnGlyHisProAspLeuGlnLysAspThrSerLysAsnAlaTyrThr 520  
Db AACCGGACCTTCCAGGGCCATCCAGATTTCAGAAAGGACACATCAAAAAATGSCCTGGAAT 1893  
QY AspThrLysValLysLysAsnSerAspAlaSerAspAsnAlaHisSerValLysGlnGln 540  
Db GATCAAAAAGTCAAAAAGAACTCTGATGCTTCTGATAATGACATCTCTGTAACACGCAA 1953  
QY AsnThrMetLysTyrMetThrAlaLeuHisSerLysProGluIleLeuGlnGlnCys 560  
Db AATACCATGAAATATATGACTGCACTTCACAGTAAACCTGAGATAAATCCAAACAAGAAATG 2013  
QY ValPheGlySerAspProLeuSerGluGlnSerLysThrArgGlyMetGluProProTyr 580  
Db GTTTTGGCTCAGATCCCTCTTTCTGAACAGAGCAAGACTAGGGGTATGGAGCCACCATGG 2073  
QY GlyTyrGlnAsnArgThrLeuArgSerIleThrSerProLeuValAlaHisArgLeuLys 600  
Db GGTATCAGAAATCGTACATTAAGAGCAATTAATCTCGTTGGTTGCTCAGAGTTAAA 2133  
QY ProfileArgGlnLysThrLysLysAlaValValSerIleLeuAspSerGluGluValCys 620  
Db CCAATCAGACAGAAAAACAAAAGCGCTGGTGAGCATACTTGATTCAGAGGAGGTGTGT 2193  
QY ValGluLeuValLysGluTyrAlaSerGlnGluTyrValLysGluValLeuGlnIleSer 640  
Db GTGAGGCTTGTAAAGGAGTATGCATCTCAAGAAATATGTGAAGAAGTTCCTTCAGATATCT 2253  
QY SerAspGlyAsnThrIleThrIleTyrTyrProAsnGlyGlyArgGlyPheProLeuAla 660  
Db AGTGATGGAATACGATCACTATTTATATCCAAATGGTGGTAGAGGTTTCTCTTGTCT 2313  
QY AspArgProSerProThrAspAsnIleSerArgTyrSerPheAspAsnLeuProGlu 680  
Db GATAGACACCCCTCACCTACTACAAACATCAGTAGGTACAGCTTTGACAAATTTACCAGAA 2373  
QY LysTyrTyrAspGlySerGlnTyrAlaSerArgPheValGlnLeuValArgSerLysSer 700  
Db AAATACTGGCGAAATATCAATATGCTTCCAGGTTTGACAGCTTGTAAAGATCTAAATCT 2433  
QY ProLysIleThrTyrPheThrArgTyrAlaLysCysIleLeuMetGluAsnSerProGly 720  
Db CCCAAATCACTTATTTTACAAGATATGCTAAATGCAATTTTATGATGGAGAAATCTCCTGCT 2493  
QY AlaAspPheGluValTyrPheTyrAspGlyValLysIleHisLysThrGluAspPheIle 740  
Db GCTGATTTGAGGTTTGGTTTTATGATGGGGTAAAAATACACAAAACAGAAAGATTTCAAT 2553  
QY GlnValIleGluLysThrGlyLysSerTyrThrLeuLysSerGluSerGluValAsnSer 760  
Db CAGGTGATTGAAAAGACAGGGAAGTCTTTACACTTTAAAAAGTGAAGTGAAGTAAATAGC 2613  
QY LeuLysGluGluIleLysMetTyrMetAspHisAlaAsnGluGlyHisArgIleCysLeu 780  
Db TTGAAAGAGGAGATAAAAATGATATGACCATGCTAATGAGGGTCATCGTATTTGTTA 2673  
QY AlaLeuGluSerIleIleSerGluGluArgLysThrArgSerAlaProPhePhePro 800  
Db GCATCGGAATCCATAATTTTCAAGAGAGAAAGGAAAACTAGGAGGTGCTCCCTTTTCCCA 2733  
QY IleIleIleGlyArgLysProGlySerThrSerProLysAlaLeuSerProProPro 820  
Db ATATCATAGGAAGAAAAACCTGGTAGTACTAGTTCACTTAAGGCTTATCACTCTCTCT 2793  
QY SerValAspSerAsnTyrProThrArgAspArgAlaSerPheAsnArgMetValMethis 840  
Db TCTGTGGATTCAAATTTACCAACAGAGAGATAGAGCATCTTTCAACAGAAATGGTCTGAT 2853

QY 841 SerAlaAlaSerProThrGlnAlaProIleLeuAsnProSerMetValThrAsnGluGly 860  
DB 2854 AGTGGCTGCTTCCACACAGAGCCCAATCCTTAATCCCTCTATGGTTACAAATGAAGGA 2913  
QY 861 LeuGlyLeuThrThrAlaSerGlyThrAspIleSerSerAsnSerLeuLysAspCys 880  
DB 2914 CTTGGCTTACAACTACAGCTTCTGGACAGACATCTCTTAATAGTCTAAAGATTGT 2973  
QY 881 LeuProLysSerAlaGlnLeuLeuLysSerValPheValLysAsnValGlyTrpAlaThr 900  
DB 2974 CTTCTCTAAATCAGCAACATTTTGAATCTGTTTTGTGAAAAATGTTGGTTGGGTACA 3033  
QY 901 GlnLeuThrSerGlyAlaValTrpValGlnPheAsnAspGlySerGlnLeuValGln 920  
DB 3034 CAGTTAACTAGTGGAGCTGTGGGTTCAGTTTAATGATGGGTGCCAGTTGTTGCCAG 3093  
QY 921 AlaGlyValSerSerIleSerIleThrSerProAsnGlyGlnThrThrArgTrpGlyGlu 940  
DB 3094 GCAGGAGTGCTTCTATCATGATTATACCTCACCATAATGGTCAAACTAGGTATGGAGAA 3153  
QY 941 AsnGluLysLeuProAspTrpIleLysGlnLysLeuGlnCysLeuSerSerIleLeuLeu 960  
DB 3154 AATGAAAAATACCAGACTACATCAACACAGAAAAATTACAGTGTCTGTCTTCCATCCTTTTG 3213  
QY 961 MetPheSerAsnProThrProAsnPheHis 970  
DB 3214 ATGTTTTCTTAATCCGACTCCTTAATTTTCAT 3243

## RESULT 3

US-10-117-722-280  
; Sequence 280, Application US/10117722  
; Publication No. US20030219744A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Zhang, Jie  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. US20030219744A1el Nucleic Acids and  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 784CIP28CIP  
; CURRENT APPLICATION NUMBER: US/10/117,722  
; CURRENT FILING DATE: 2002-04-04  
; PRIOR APPLICATION NUMBER: 09/620,312  
; PRIOR FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 1104  
; SOFTWARE: pt\_FL\_genes Version 1.0  
; SEQ ID NO 280  
; LENGTH: 3937  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (334)..(3246)  
US-10-117-722-280

## Alignment Scores:

Pred. No.: 0 Length: 3937  
Score: 5075.00 Matches: 969  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.90% Mismatches: 0  
Query Match: 99.94% Indels: 0  
DB: 17 Gaps: 0

US-10-026-021-2 (1-970) x US-10-117-722-280 (1-3937)

QY 1 MetAlaThrCysIleGlyLysIleGluAspPheLysValGlyAsnLeuLeuGlyLys 20  
DB 334 ATGGCGACCTGCATCGGGGAGAGATCGAGGATTTTAAAGTTTGAAGTCTGCTTGTGTTAA 393

QY 21 GlySerPheAlaGlyValTyArgAlaGluSerIleHisThrGlyLeuGluValAlaIle 40  
DB 334 GGAATCATTTGCTGGTGTCTACAGAGCTGAGTCCATTCACACTGGTTTGGAGTTGCAATC 453  
QY 41 LysMetIleAspLysLeuAlaMetTyLysAlaGlyMetValGlnArgValGlnAsnGlu 60  
DB 454 AAAATGATAGATAAGAAAGCCATGTACAAAGCAGGAATGGTACAGAGAGTCCAAATGAG 513  
QY 61 ValLysIleHisCysGlnLeuLysHisProSerIleLeuGluLeuTyAsnTrpPheGlu 80  
DB 514 GTGAAATACATTCGCAATTCGAACATCTTCTATCTTGGAGCTTTATACTATTTTGAA 573  
QY 81 AspSerAsnTrpValTyLeuValLeuGluMetCysHisAsnGlyGluMetAsnArgTrp 100  
DB 574 GATACCAATTATGTGTATCTGTATTAAGAAATGTGCCAATATGGCAAGAAATGAACAGGTAT 633  
QY 101 LeuLysAsnArgValLysProPheSerGluAsnGluAlaArgHisPheMetHisGlnIle 120  
DB 634 CTAAGAAATAGAGTGAACCCCTTCTCAGAAATGAAGCTCGACACTTCATGCACCAGATC 693  
QY 121 IleThrGlyMetLeuTyLysLeuHisSerHisGlyIleLeuHisArgAspLeuThrLeuSer 140  
DB 694 ATCAGAGGATGTGTATCTTCTCATCTGTATCTACACCGGGAACCTCACACTTCT 753  
QY 141 AsnLeuLeuLeuThrArgAsnMetAsnIleLysIleAlaAspPheGlyLeuAlaThrGln 160  
DB 754 AACCTCTACTGACTCGTAATATGAACATCAAGATTGTGATTTTGGGTGGCAACTCAA 813  
QY 161 LeuLysMetProHisGluLysHisTyThrLeuCysGlyThrProAsnTrpIleSerPro 180  
DB 814 CTGAAATGGCCACATGAAAGCCTATATATGTGGAACCTCTTAACCTACACTTTCCACA 873  
QY 181 GluIleAlaThrArgSerAlaHisGlyLeuGluSerAspValTrpSerLeuGlyCysMet 200  
DB 874 GAATTTGCCACTCGAAGTGCATGGCCCTTGAATCTGTATGTTTGGTCTCTGGCTGTATG 933  
QY 201 PheTyThrLeuLeuIleGlyArgProPheAspThrAspThrValLysAsnThrLeu 220  
DB 934 TTTTATACATTACTTATCGGAGAGACCCCTTCGACACTGCACAGTCAAGAAACACATTA 993  
QY 221 AsnLysValValLeuAlaAspTyTrpGluMetProSerPheLeuSerIleGluAlaLysAsp 240  
DB 994 AATAAGTAGTATTTGGCAGATTTATGAAATGCCAATCTTTTGTCAATAGAGCCCAAGGAC 1053  
QY 241 LeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeuSerLeuSerValLeu 260  
DB 1054 CTTATTCACAGTACTTCTCGTAGAAATCCAGCAGATCGTTTAAGTCTGTCTTCAGTATG 1113  
QY 261 AspHisProPheMetSerArgAsnSerSerThrLysSerLysAspLeuGlyThrValGlu 280  
DB 1114 GACCATCTTTTATGTCTCCGAAATTTCTTCAACAAAAAGTAAAGATTAGGAACCTGGAA 1173  
QY 281 AspSerIleAspSerGlyHisAlaThrIleSerThrAlaIleThrAlaSerSerThr 300  
DB 1174 GACTCAATTGATAGTGGGCATGCCAATTTCTACTGCAATTTACAGCTTTCTTCCAGTACC 1233  
QY 301 SerIleSerGlySerLeuPheAspLysArgArgLeuLeuIleGlyGlnProLeuProAsn 320  
DB 1234 AGTATAAGTGTAGTTTATTTGACAAAAAGAGACTTTTGAATTTGGTCAGCCACTCCCAAT 1293  
QY 321 LysMetThrValPheProLysAsnLysSerSerThrAspPheSerSerSerGlyAspGly 340  
DB 1294 AAAATGACTGTATTTCCAAAGATAAAAGTTCACTGATTTTCTTCTTCAGGAGATGGA 1353  
QY 341 AsnSerPheTyThrGlnTrpGlyAsnGlnGluThrSerAsnSerGlyArgGlyVal 360  
DB 1354 AACAGTTTTTATCTCAGTGGGGAATCAAGAAACAGTAAATAGTGGGAAGGGAAGATA 1413  
QY 361 IleGlnAspAlaGluGluArgProHisSerArgTyLeuArgArgAlaTySerSerAsp 380  
DB 1414 ATTCAGATGCAGAAAGAAAGGCCACATTTCTCGATACCTTCGTAGAGCTTATTTCTCTGAT 1473

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QY 381 ArgSerGlyThrSerAsnSerGlnSerGlnAlaLysThrTyrThrMetGluArgCysHis 400
Db 1474 AGATCTGGCACCTCTTAATAGTCAGTCTCAAGCAAAACATATACAAATGGAACGATGTCAC 1533
QY 401 SerAlaGluMetLeuSerValSerLysArgSerGlyGlyGlyGluAsnGluGluArgTyr 420
Db 1534 TCAGCAGAAATGCTTTCAGTCTCCAAAGATCAGGAGGAGGTGAAATGAAGAGAGGTAC 1593
QY 421 SerProThrAspAsnAlaAsnAlaAsnLeuPheAsnPheLysGluLysThrSerSerSer 440
Db 1594 TCACCACACAGACAAATGCCAACATTTTAACTCTTTAAAGAAAAGACATCCAGTAGT 1653
QY 441 SerGlySerPheGluArgProAspAsnGlnAlaLeuSerAsnHisLeuCysProGly 460
Db 1654 TCTGGATCTTTTGAAGAGCCTCATTAACAATCAAGCACTCTCCAATCATCTTTGTCCAGGA 1713
QY 461 LysThrProPheProPheAlaAspProThrProGlnThrGluThrValGlnGlnTrpPhe 480
Db 1714 AAAACTCTCTTTCCATTTCAGACCCGACACTTCAGACTGAAAACCGTACACAGTGGTTT 1773
QY 481 GlyAsnLeuGlnLeuAsnAlaHisLeuArgLysThrThrGluTyrAspSerIleSerPro 500
Db 1774 GGGAAATCTGCAATAAATGCTCATTTAAGAAAAAATCTACTGAATATGACAGCATCAGCCCA 1833
QY 501 AsnArgAspPheGlnGlyHisProAspLeuGlnLysAspThrSerLysAsnAlaTrpThr 520
Db 1834 AACCGGAGCTTCAGGGCCATCCAGATTTGCAAGAGGACACATCAAAAAAATCCCTGGACT 1893
QY 521 AspThrLysValLysLysAsnSerAspAlaSerAspAsnAlaHisSerValLysGlnGln 540
Db 1894 GATACAAAAGTCAAAGAAGCTCTGATGCTTCTGATATGACATCTCTGTAAGACGAA 1953
QY 541 AsnThrMetLysTyrMetThrAlaLeuHisSerLysProGluLeuIleGlnGlnCys 560
Db 1954 AATACCATGAAATATATGACTGCACCTTCACAGTAAACCTGAGATAATCCAAACAAGATGT 2013
QY 561 ValPheGlySerAspProLeuSerGluGlnSerLysThrArgGlyMetGluProTrp 580
Db 2014 GTTTTGGCTCAGATCCTCTTTCTGAACAGAGCAAGACTAGGGGTATGGAGCCACCATGG 2073
QY 581 GlyTyrGlnAsnArgThrLeuArgSerIleThrSerProLeuValAlaHisArgLeuLys 600
Db 2074 GGTATCAGAAATCGTACATTAGAGCAATTAATCTCCGTTGGTGTCTCAGAGTTAAA 2133
QY 601 ProIleArgGlnLysThrLysLysAlaValValSerIleLeuAspSerGluGluValCys 620
Db 2134 CCAATCAGACAGAAAAACCAAAAGGCTGTGGTGAGCATACTTGTATTCAGAGGAGGTGT 2193
QY 621 ValGluLeuValLysGluTyrAlaSerGlnGlnTyrValLysGluValLeuGlnIleSer 640
Db 2194 GTGGAGCTTGTAAAGGAGTATGCATCTCAAGAAATATGTGAAGAAAGTTCTTCAGATATCT 2253
QY 641 SerAspGlyAsnThrIleThrIleTyrTyrProAsnGlyGlyArgGlyPheProLeuAla 660
Db 2254 AGTGATGGAATACGATCACTATTATTATCCAAATGGTGGTAGAGTTTCTCTTGTCT 2313
QY 661 AspArgProProSerProThrAspAsnIleSerArgTyrSerPheAspAsnLeuProGlu 680
Db 2314 GATAGACCACTTCACTACTGACAAACATCAGTAGGTACAGCTTTGACAAATTTACAGAA 2373
QY 681 LysTyrTrpArgLysTyrGlnTyrAlaSerArgPheValGlnLeuValArgSerLysSer 700
Db 2374 AAATACTGGCGAAAATATCAATATGCTTCCAGGTTTGTACAGCTTGTAAAGATCTAAATCT 2433
QY 701 ProLysIleThrTyrPheThrArgTyrAlaLysCysIleLeuMetGluAsnSerProGly 720
Db 2434 CCCAAATCACTATTATTTACAGATATGCTTAATGCATTTTGTATGGAGATTTCTCTGT 2493
QY 721 AlaAspPheGluValTrpPheTyrAspGlyValLysIleHisLysThrGluAspPheIle 740
Db 2494 GCTGATTTTGGGTTTGGTTTATGATGGGTAAAAATACACAAACAGAGATTTTCATT 2553
QY 741 GlnValIleGluLysThrGlyLysSerTyrThrLeuLysSerGluSerGluValAsnSer 760
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Db 2554 CAGGTGATTGAAAAGACAGGAAGTCTTACACTTTTAAAAAGTGAAGTGAAGTAAATAGC 2613
QY 761 LeuLysGluGluIleLysMetTyrMetAspHisAlaAsnGluGlyHisArgIleCysLeu 780
Db 2614 TTGAAAGAGGAGATAAAAATGATATGGACCATCTAATAGAGGTTCATCGTATTGTTTA 2673
QY 781 AlaLeuGluSerIleLysSerGluGluArgLysThrArgSerAlaProPhePhePro 800
Db 2674 GCATCGGAATCCATAATTTTCAAGAGAGAAAGGAAAACTAGGAGTGTCTCCCTTTTCCCA 2733
QY 801 IleIleIleGlyArgLysProGlySerThrSerSerProLysAlaLeuSerProProPro 820
Db 2734 ATAATCATAGGAAGAAACCTGGTAGTACTAGTTCACTTAAGGGCTTATACCTCCCTCT 2793
QY 821 SerValAspSerAsnTyrProThrArgAspArgAlaSerPheAsnArgMetValMetHis 840
Db 2794 TCTGTGGATTCAAAATTACCCAAACGAGAGATAGAGCACTTTTCAACAGAAATGTCATGCAT 2853
QY 841 SerAlaAlaSerProThrGlnAlaProIleLeuAsnProSerMetValThrAsnGluGly 860
Db 2854 AGTGTGCTTCTCCAAACACAGGCCCAATCCTTAATCCCTCTATGTTTACAAATGAAGGA 2913
QY 861 LeuGlyLeuThrThrThrAlaSerGlyThrAspIleSerSerAsnSerLeuLysAspCys 880
Db 2914 CTTGTGCTCTTCAACTCAGACTTCTGGAAACAGACATCTCTCTAATAGTCTTAAAAAGATTGT 2973
QY 881 LeuProLysSerAlaGlnLeuLeuLysSerValPheValLysAsnValGlyTrpAlaThr 900
Db 2974 CTTCTTAATCAGCACAACTTTTGAATCTGTTTTTGTGAAAAATGTTGGTTGGCTACA 3033
QY 901 GlnLeuThrSerGlyAlaValTrpValGlnPheAsnAspGlySerGlnLeuValValGln 920
Db 3034 CAGTTAACTAGTGAGCTGTGTGGGTTCAGTTTAATGATGGGTCCAGTTCGTTGTGCAG 3093
QY 921 AlaGlyValSerSerIleSerTyrThrSerProAsnGlyGlnThrArgTyrGlyGlu 940
Db 3094 GCAGAGGTGCTTCTATCAGTTATACCTTCAACAAATGGTCAACAACTAGGTATGGAGAA 3153
QY 941 AsnGluLysLeuProAspTyrIleLysGlnLysLeuGlnCysLeuSerSerIleLeuLeu 960
Db 3154 AATGAAAAATTACAGACTACATCAACAGAAAATTCAGTGTCTGTCTTCCATCTTTTG 3213
QY 961 MetPheSerAsnProThrProAsnPheHis 970
Db 3214 ATGTTTCTAATCCGACTCCTTAATTTTCAT 3243

RESULT 4
US-10-116-802-108
; Sequence 108, Application US/10116802
; Publication No. US20030065157A1
; GENERAL INFORMATION:
; APPLICANT: Amy Lasek
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0045 US
; CURRENT APPLICATION NUMBER: US/10/116,802
; PRIORITY FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,593
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 519
; SOFTWARE: PERL Program
; SEQ ID NO 108
; LENGTH: 3721
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 492750CB1
US-10-116-802-108

Alignment Scores:
Pred. No.: 0 Length: 3721
Score: 5071.00 Matches: 968
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Percent Similarity:	100.00%	Conservative:	2
Best Local Similarity:	99.79%	Mismatches:	0
Query Match:	99.86%	Indels:	0
DB:	14	Gaps:	0
US-10-026-021-2 (1-970) x US-10-116-802-108 (1-3721)			
QY	1	MetAlaThrCysIleGlyGluLysIleGluAspPheLysValGlyAsnLeuLeuGlyLys	20
DB	288	ATGGCCACCTGTCATCGGGGAGAGATCGAGGATTTTAAAGTTGGAATCTGCTTGGTAAA	347
QY	21	GlySerPheAlaGlyValTyrArgAlaGluSerIleHisThrClyLeuGluValAlaIle	40
DB	348	GGATCAATTTGCTGTCTACAGAGCTGAGTCCATTCACACTGGTTTGAAGTTGCAATC	407
QY	41	LysMetIleAspLysLysAlaMetTyrLysAlaGlyMetValGlnArgValGlnAsnGlu	60
DB	408	AAATGATAGATAAGAAAGCCATGTACAAAGCAGGATGTTGACAGAGTCAAAATGAG	467
QY	61	ValLysIleHisCysGlnLeuLysHisProSerIleLeuGluLeuTyrAsnTyrPheGlu	80
DB	468	GTGAAATACATTCGCAATTGAAACATCTCTATCTTGGAGCTTTATTAATATTTTGAA	527
QY	81	AspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsnGlyClyuMetAsnArgTyr	100
DB	528	GATAGCAATTTATGTGTATCTGTTATTAAGAAATGTCCATAATGGAGAAATGAACAGGTAT	587
QY	101	LeuLysAsnArgValLysProPheSerGluAsnGluAlaArgHisPheMetHisGlnIle	120
DB	588	CTAAGAAATAGATGAAACCTTCTCAGAAATGAAGCTCGACACTTCATGCACAGATC	647
QY	121	IleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHisArgAspLeuThrLeuSer	140
DB	648	ATCAGAGGATGTTGTATCTTCATCTCATGTGTATACACCGGACCTCACACTTCT	707
QY	141	AsnLeuLeuLeuThrArgAsnMetAsnIleLysIleAlaAspPheGlyLeuAlaThrGln	160
DB	708	AACTCTCTACTGACTCGTAATATGAACATCAAGATTTGCTGATTTGGCCCTGGCACTCAA	767
QY	161	LeuLysMetProHisGlyLysHisTyrThrLeuCysGlyThrProAsnTyrIleSerPro	180
DB	768	CTGAAATGCCATGAAAGACATATACATTATGTGGAACTCTCTAACTACATTTCCACCA	827
QY	181	GluIleAlaThrArgSerAlaHisGlyLeuGluSerAspValTyrSerLeuGlyCysMet	200
DB	828	GAAATTTGCCACTCGAAGTGCACATGCGCTTTGAATCTGATGTTGGTCCCTGGCTGTATG	887
QY	201	PheTyrThrLeuLeuIleGlyArgProPheAspThrAspThrValLysAsnThrLeu	220
DB	888	TTTTATACATTTACTATCGGGAGACCACCTTCGACACTGCACACAGTCAAGAACACATTA	947
QY	221	AsnLysValValLeuAlaAspTyrGluMetProSerPheLeuSerIleGluAlaLysAsp	240
DB	948	AATAAGTAGTAGTGGCAATATGAATGCCAACTTTTGTCAATAGAGGCCAAGGAC	1007
QY	241	LeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeuSerLeuSerValLeu	260
DB	1008	CTTATTCACAGTACTCTGTAGAAATCCAGCAGATCGTTTAAGTCTGTCTTCAGTATTTG	1067
QY	261	AspHisProPheMetSerArgAsnSerSerThrLysSerLysAspLeuGlyThrValGlu	280
DB	1068	GACCATCTCTTTATGTGTCGCAATCTTCAACAAAGATTAAGATTTAGGAATCTGGAA	1127
QY	281	AspSerIleAspSerClyHisAlaThrIleSerThrAlaIleThrAlaSerSerSerThr	300
DB	1128	GACTCAATTTGATGGGATGCCCAATTTCTACTGCAATTTACAGCTTCTTCCAGTACC	1187
QY	301	SerIleSerGlySerLeuPheAspLysArgGluLeuIleGlyClnProLeuProAsn	320
DB	1188	AGTATAAGTGTAGTTTATTTGACAAAGAGACTTTTGTGTTGTCAGCCACTCCCAAT	1247
QY	321	LysMetThrValPheProLysAsnLysSerSerThrAspPheSerSerSerGlyAspGly	340

DB	1248	AAAATGACTGTATTTTCCAAAGAATAAAAGTTTCAACTGATTTTCTTCTTCCAGGATGGA	1307
QY	341	AsnSerPheTyrThrGlnTyrGlyAsnGlnGluThrSerAsnSerGlyArgGlyVal	360
DB	1308	AACAGTTTTTATCTCAGTGGGGAATCAAGAAACAGTATATAGTGAAGGAGAGTA	1367
QY	361	IleGlnAspAlaGluGluArgProHisSerArgTyrLeuArgArgAlaTyrSerSerAsp	380
DB	1368	ATTCAAGATGCAGAAAGAGGCCACATTTCTCGATACCTTCGTAGAGCTTATTTCTCTGAT	1427
QY	381	ArgSerGlyThrSerAsnSerClnSerGlnAlaLysThrTyrMetClnArgCysHis	400
DB	1428	AGATCTGGCACTTCTAATAGTCAGTCTCAAGCAAAACATATACAAATGGAACGATGTAC	1487
QY	401	SerAlaGluMetLeuSerValSerLysArgSerGlyGlyGlyGluAsnGluGluArgTyr	420
DB	1488	TCAGCAGAAATGCTTTTCAAGTGTCCAAAGATCAGGAGGAGTGAANAATGAGAGGATAC	1547
QY	421	SerProThrAspAsnAsnAlaAsnIlePheAsnPheLysGlyLysThrSerSerSer	440
DB	1548	TCACCCACAGACAAACATGCCAACATTTTAACTTCTTTAAAGAAAGACATCCAGTAGT	1607
QY	441	SerGlySerPheGluArgProAspAsnAsnGlnAlaLeuSerAsnHisLeuCysProGly	460
DB	1608	TCTGGATCTTTTGAAGACCTGATAACAATCAAGCACTCTCCAATCATCTTTGTCCAGGA	1667
QY	461	LysThrProPhePheAlaAspProThrProGlnThrGluThrValGlnGlnTyrPhe	480
DB	1668	AAATCTCTTTTCCATTTTGCAGCCGACCTCAGACTGAAACCGTACACAGTGGTTT	1727
QY	481	GlyAsnLeuGlnIleAsnAlaHisLeuArgLysThrGluTyrAspSerIleSerPro	500
DB	1728	GGGAATCTGCAAAATAAATGCTCATTTAAGAAAACTACTGAATATGACACATCAGCCCA	1787
QY	501	AsnArgAspPheGlnGlyHisProAspLeuGlnLysAspThrSerLysAsnAlaTyrThr	520
DB	1788	AACCGGACTTCCAGGGCCATCCAGATTTCGAGAGGACACATCAAAAAATGCTGGACT	1847
QY	521	AspThrLysValLysLysAsnSerAspAlaSerAspAsnAlaHisSerValLysGlnGln	540
DB	1848	GATACAAAGTCAAAAAGAACTCTGATGCTTCTGATAATGCACATCTGTAAACAGCAA	1907
QY	541	AsnThrMetLysTyrMetThrAlaLeuHisSerLysProGluIleIleGlnGlnCys	560
DB	1908	AATACCATGAAATATATGACTGCATTCACAGTAAACCTGAGATAATCCACAGAATGT	1967
QY	561	ValPheGlySerAspProLeuSerGlnSerLysThrArgGlyMetGluProProIle	580
DB	1968	GTTTTGGCTCAGATCTCTTTCTGAACAGAGCAGACTAGGGGTATGGAGCCACATGG	2027
QY	581	GlyTyrGlnAsnArgThrLeuArgSerIleThrSerProLeuValAlaHisArgLeuLys	600
DB	2028	GGTATATCAGATCGTACATTAAGAGCAATACATCTCCGTGGTTGGTCTCACAGGTTAAAA	2087
QY	601	ProIleArgGlnLysThrLysLysAlaValValSerIleLeuAspSerGluGluValCys	620
DB	2088	CCAATCAGACAGAAAAACCAAAAGGCTGTGGTGAGCATACTTGATTCAGAGGAGGTGT	2147
QY	621	ValGluLeuValLysGluTyrAlaSerGlnGluTyrValLysGluValLeuGlnIleSer	640
DB	2148	GTGGAGCTGTAAAGGAGTATGATCTCAAGATATGTGAAAGAAAGTTCTTTCAGATATCT	2207
QY	641	SerAspGlyAsnThrIleThrIleTyrTyrProAsnGlyGlyArgGlyPheProLeuAla	660
DB	2208	AGTGATGAAATACCATCATTTATTTATCCAAATGGTGTAGAGGTTTCTCTCTTCT	2267
QY	661	AspArgProProSerProThrAspAsnIleSerArgTyrSerPheAspAsnLeuProGlu	680
DB	2268	GATAGCACCCCTCACCCTACTGACAAACATCAGTAGGTACAGCTTTGACATTTACCAGA	2327
QY	681	LysTyrIlePheArgLysTyrGlnTyrAlaSerArgPheValGlnLeuValArgSerLysSer	700
DB	2328	AAATACTGGCAAAATATCAATATGCTTCCAGGTTTGTACAGCTTGTGAAGATCTAAATCT	2387

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QY 701 ProLysIleThrTyrPheThrArgTyrAlaLysCysIleLeuMetGluAsnSerProGly 720
Db 2388 CCCAAATCACCATTATTTTACAGATATGCTAAATGCATTTTATGATGAGAAATCTCTCTGT 2447
QY 721 AlaAspPheGluValTyrPheTyrAspGlyValLysIleHisLeuThrGluAspPheIle 740
Db 2448 GCTGATTTGAGTTTGGTTTATGATGGGGTAAATACAAACAGAGATTCAT 2507
QY 741 GlnValIleGluLysThrGlyLysSerTyrThrLeuLysSerGluSerGluValAsnSer 760
Db 2508 CAGGTGATTTGAAAGACAGCGAAGTCTTACACTTTTAAAGTGAAGTGAAGTAAATAGC 2567
QY 761 LeuLysGluGluIleLysMetTyrMetAspHisAlaAsnGluGlyHisArgIleCysLeu 780
Db 2568 TTGAAAGAGAGATATAAAATGATATGGACCATGCTAATGAGGGTCATCGTATTTGTTTA 2627
QY 781 AlaLeuGluSerIleLeuSerGluGluArgLysThrArgSerAlaProPhePro 800
Db 2628 GCATGGATCCATATTTACAGAGAGGAAAGAACTAGAGTGCTCCCTTTTCCCA 2687
QY 801 IleIleIleGlyArgLysProGlySerThrSerProLysAlaLeuSerProPro 820
Db 2688 ATAATCATAGGAAGAAACCTGGTAGTACTAGTTCACCTTAAGGCTTATCACCTCCTCT 2747
QY 821 SerValAspSerAsnTyrProThrArgAspArgAlaSerPheAsnArgMetValMetHis 840
Db 2748 TCTGTGGATTTCAAAATTACCAACGAGATAGAGCATCTTTCAACAGAAATGGTCATGCAT 2807
QY 841 SerAlaAlaSerProThrGlnAlaProIleLeuAsnProSerMetValThrAsnGluGly 860
Db 2808 AGTGTGCTTCTCCACACAGGACCAATCCCTTATCCCTCATGTTTACAAATGAAGA 2867
QY 861 LeuGlyLeuThrThrAlaSerGlyThrAspIleSerSerAsnSerLeuLysAspCys 880
Db 2868 CTTGTGCTTACAACTACAGCTTCTGGAACAGACATCTCTTAATAGTCTAAAGATTGT 2927
QY 881 LeuProLysSerAlaGlnLeuLysSerValPheValLysAsnValGlyTrpAlaThr 900
Db 2928 CTTCTTAATACAGCAACTTTGAAATCTGTTTTTGTGAAAAATGTTGGTTGGGCTACA 2987
QY 901 GlnLeuThrSerGlyAlaValTyrValGlnPheAsnAspGlySerGlnLeuValGln 920
Db 2988 CAGTTAACTAGTGGAGCTGTGGTTCAGTTTAATGATGGTCCAGTTGGTTGGCAG 3047
QY 921 AlaGlyValSerSerIleSerTyrThrSerProAsnGlyGlnThrThrArgTyrGlyGlu 940
Db 3048 GCAGGAGTGCTTCTATCATGTTATACCTCACCAAATGGTCAAACTAGGTATGGAGAA 3107
QY 941 AsnGluLysLeuProAspTyrIleLysGlnLysLeuGlnCysLeuSerSerIleLeuLeu 960
Db 3108 AATGAAAAATTACAGACTACATCAACAGAAATTACAGTGCTGTCTCTCCATCCTTTTG 3167
QY 961 MetPheSerAsnProThrProAsnPheHis 970
Db 3168 ATGTTTCTTAATCCGACTCCTAATTTTCAT 3197
RESULT 5
US-10-737-450-89
; Sequence 89, Application US/10737450
; Publication No. US20040235071A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Lightcap, Eric S.
; APPLICANT: Ecsedy, Jeffrey A.
; APPLICANT: Hunter, John Joseph
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Tighe Nestor, Michelle
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 15986, 2188, 20743, 9148, 9151, 9791, 44252,
; TITLE OF INVENTION: 14184, 42461, 8204, 7970, 25552, 21657, 26492, 2411, 15088,
; TITLE OF INVENTION: 1905, 28899, 63380, 33935, 10480, 12686, 25501, 17694,
; TITLE OF INVENTION: 15701, 53062, 49908, 21612, 38949, 6216, 46863, 9235, 2201,
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; TITLE OF INVENTION: 6985, 9883, 12238, 18057, 21617, 39228, 49928, 54476, 62113,
; TITLE OF INVENTION: 64316, 12264, 32362, 58198, 2887, 3205, 8557, 9600, 9693,
; TITLE OF INVENTION: 44867, 53058, 55556, 57658, 2208, 10252, 10302, 14218,
; TITLE OF INVENTION: 33877, 10317, 10485, 25964, 14815, 1363, 1397, 14827, 21708,
; TITLE OF INVENTION: 3803, 64698, 2179 OR 13249
; FILE REFERENCE: MPI02-207P1RNMNIM
; CURRENT APPLICATION NUMBER: US/10/737,450
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/435,108
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/436,443
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/438,498
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/444,370
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 60/446,031
; PRIOR FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: US 60/453,635
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/457,199
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/462,458
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 60/466,732
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/469,184
; PRIOR FILING DATE: 2003-05-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 3092
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (141)...(3053)
US-10-737-450-89
Alignment Scores:
Pred. No.: 0 Length: 3092
Score: 5067.00 Matches: 967
Percent Similarity: 100.00% Conservative: 3
Best Local Similarity: 99.69% Mismatches: 0
Query Match: 99.78% Indels: 0
DB: 20 Gaps: 0
US-10-026-021-2 (1-970) x US-10-737-450-89 (1-3092)
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QY 21 GlySerPheAlaGlyValTyrArgAlaGluSerIleHisThrGlyLeuGluValAlaIle 40
Db 201 GGATCATTTGCTGTGTTCTACAGAGCTGAGTCCATTCACACTGGTTTGGAAAGTTGCAATC 260
QY 41 LysMetIleAspLysLysAlaMetTyrLysAlaGlyMetValGlnArgValGlnAsnGlu 60
Db 261 AAAATGATAGATAGAAAGCCATGTCANACAGAGATGGTACAGAGAGTCAAAAATGAG 320
QY 61 VallysIleHisCysGlnLeuLysHisProSerIleLeuGluLeuTyrAsnTyrPheGlu 80
Db 321 GTGAAAAATACATTGCCAATTCGAAACATCTCTATCTTGGAGCTTTATAACTATTTTCAA 380
QY 81 AspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsnGlyGluMetAsnArgTyr 100
Db 381 GATAGCAATTAATGTTATCTGGTATTGAAATATGCCATAATGGAGAAATGAACAGGTAT 440
QY 101 LeuLysAsnArgValLysProPheSerGluAsnGluAlaArgHisPheMetHisGlnIle 120
Db 441 CTAAAGATAGAGTGAAACCCCTTCTCGAAATAGAGCTTCGACACTTCATTCACACCATC 500
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121 IleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHisArgAspLeuThrLeuSer 140  
501 ATCACAGGATGTTGATCTTCAATCTCATGTTATACACCGGACCTCACACTTCT 560  
141 AsnLeuLeuThrArgAsnMetAsnIleLysIleAlaAspGlyLeuAlaThrGln 160  
561 AACCTCCCTACTACCTCGTAATATGAACATCAAGATTGCTGATTTTGGGCTGGCACTCAA 620  
161 LeuLysMetProHisGlyLysHisTyrThrLeuCysGlyThrProAsnTyrIleSerPro 180  
621 CTGAAATGCCACATGAAAGACATATACATTTATGTGGACCTCCCTAACATTTACACA 680  
181 GluIleAlaThrArgSerAlaHisGlyLeuGluSerAspValTyrSerLeuGlyCysMet 200  
681 GAAATTTGCCACTCGAAGTGCATGGCTTGAATCTGATGTTTGGTCCCTGGGCTGTATG 740  
201 PheTyrThrLeuLeuIleGlyArgProProPheAspThrAspThrValLysAsnThrLeu 220  
741 TTTTATACATTAATCTATCGGGAGACCCCTTCGACACCTGACACAGTCAAGAACACATTA 800  
221 AsnLysValValLeuAlaAspTyrGluMetProSerPheLeuSerIleGluAlaLysAsp 240  
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241 LeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeuSerLeuSerSerValLeu 260  
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261 AspHisProPheMetSerArgAsnSerSerThrLysSerLysAspLeuGlyThrValGlu 280  
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281 AspSerIleAspSerGlyHisAlaThrIleSerThrAlaIleThrAlaSerSerSerThr 300  
981 GACTCAATTGATGGGCGATGCCAATTTCTACTGCATTTACAGTCTTTCAGTACC 1040  
301 SerIleSerGlySerLeuPheAspLysArgArgLeuLeuIleGlyGlnProLeuProAsn 320  
1041 AGTATAAGTGGTAGTTTATTTCACAAAAAGAGACTTTTGATTTGTCAGCCACTCCCAAT 1100  
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341 AsnSerPheTyrThrGlnTyrGlyAsnGlnGluThrSerAsnSerGlyArgGlyVal 360  
1161 AACAGTTTATACCTCAGTGGGGAAATCAAGAAACCCAGTAATAGTGGAGGGGAAAGAGTA 1220  
361 IleGlnAspAlaGluArgProHisSerArgTyrLeuArgArgAlaTyrSerSerAsp 380  
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381 ArgSerGlyThrSerAsnSerGlnSerGlnAlaLysThrTyrThrMetGluArgCysHis 400  
1281 AGATCTGGCACTTCTTAATAGTCAGTCTCAAGCAAAACATATACAAATGGAACGATGTAC 1340  
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1341 TCAGCAGAAATGCTTTTCAAGTGCCTCAAGAGATCAGGAGGGTGAATAATGAAGAGAGGTAC 1400  
421 SerProThrAspAsnAlaAsnIlePheAsnPhePheLysGluLysThrSerSerSer 440  
1401 TCACCCACAGACAAACATGCCAACATTTTAACTTCTTTAAGAAAGAACATCCAGTAGT 1460  
441 SerGlySerPheGluArgProAspAsnAsnGlnAlaLeuSerAsnHisLeuCysProGly 460  
1461 TCTGATCTTTTGAAGACCTGATAACAATCAAGCACTCTCCCAATCATCTTTGTCCAGGA 1520  
461 LysThrProPheProPheAlaAspProThrProGlnThrGluThrValGlnGlnTyrPhe 480  
1521 AAAAATCTCTTTTCCATTTTGCAGACCCGACACCTTCAGACTGAAACCGTACAAACAGTGGTTT 1580

481 GlyAsnLeuGlnIleAsnAlaHisLeuArgLysThrThrGluTyrAspSerIleSerPro 500  
1581 GGGAAATCTGCAATAAATGCTCATTTAAGAAAACTACTGAATATGACAGCATCAGCCCA 1640  
501 AsnArgAspPheGlnGlyHisProAspLeuGlnLysAspThrSerLysAsnAlaTyrThr 520  
1641 AACCGGACTTCCAGGGCCATCCAGATTGAGAGAGGACACATCAAAAAATGCTCGGACT 1700  
521 AspThrLysValLysLysAsnSerAspAlaSerAspAsnAlaHisSerValLysGlnGln 540  
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541 AsnThrMetLysTyrMetThrAlaLeuHisSerLysProGluIleIleGlnGlnGluCys 560  
1761 AATACCATGAATAATATGACTGCATTCACAGTAAACCTGAGATAATCCAAACAAGATGT 1820  
561 ValPheGlySerAspProLeuSerGluGlnSerLysThrArgGlyMetGluProProTyr 580  
1821 GTTTTGGCTCAGATCCTCTTCTGAACAGAGCAAGACTAGGGGTATGGGCCACCATGG 1880  
581 GlyTyrGlnAsnArgThrLeuArgSerIleThrSerProLeuValAlaHisArgLeuLys 600  
1881 GGTATCAGAAATCGTACATTAAAGACATTAATCTCCGTTGGTTGCTCAGAGGTAAAA 1940  
601 ProIleArgGlnLysThrLysLysAlaValValSerIleLeuAspSerGluGluValCys 620  
1941 CCAATCAGACAGAAAAACCAAAAGGCTGTGTGAGCATACTTGAATTCAGAGGAGGTGT 2000  
621 ValGluLeuValLysGluTyrAlaSerGlnGluTyrValLysGluValLeuGlnIleSer 640  
2001 GTGGAGCTTGTAAAGGAGTATGCATCTCAAGATATGTGAAGAAAGTTCTTCAGATATCT 2060  
641 SerAspGlyAsnThrIleThrIleTyrTyrProAsnGlyGlyArgGlyPheProLeuAla 660  
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661 AspArgProProSerProThrAspAsnIleSerArgTyrSerPheAspAsnLeuProGlu 680  
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2181 AAATACTGGCGAAATATCAATATGCTTCCAGGTTTGTACAGCTTGTAAAGATCTAAATCT 2240  
701 ProLysIleThrTyrPheThrArgTyrAlaLysCysIleLeuMetGluAsnSerProGly 720  
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721 AlaAspPheGluValTyrPheTyrAspGlyValLysIleHisLysThrGluAspPheIle 740  
2301 GCTGATTTTGAGGTTTGGTTTATGATGGGTAAAAATACACAAACAGAGAGATTTCAAT 2360  
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761 LeuLysGluGluIleLysMetTyrMetAspHisAlaAsnGluGlyHisArgIleCysLeu 780  
2421 TTGAAAGAGGAGATAAAAAATGTTTATGGACCATGCTAATGAGGGTCACTGATTTGTTA 2480  
781 AlaLeuGluSerIleIleSerGluGluGluArgLysThrArgSerAlaProPhePro 800  
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801 IleIleIleGlyArgLysProGlySerThrSerSerProLysAlaLeuSerProPro 820  
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2601 TCTGTGATTTCAAAATTTACCAACAGAGATAGAGCATCTTTCAACAGAAATGGTTCATGCA 2660  
841 SerAlaAspProThrGlnAlaProIleLeuAsnProSerMetValThrAsnGluGly 860

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Db      2661 AGTGCTGCTCTCCAAACAGCAGCCCAATCCCTTAATCCCTCTATGTTACAAATCAAGGA 2720
Qy      861 LeuGlyLeuThrThrAlaSerGlyThrAspIleSerSerAsnSerLeuLysAspCys 880
Db      2721 CTTGGTCTTACAACTACAGCTTCTCGAACAGACATCTCTCTTAATAGTCTAAAGATTGT 2780
Qy      881 LeuProLysSerAlaGlnLeuLeuLysSerValPheValLysAsnValGlyTrpAlaThr 900
Db      2781 CTTCCCTAAATACGACAACTTTGAAATCTGTTTGTGAAAAATGTTGGTTGGGCTACA 2840
Qy      901 GlnLeuThrSerGlyValaValTrpValGlnPheAsnAspGlySerGlnLeuValValGln 920
Db      2841 CAGTTAACTAGTGGAGCTGTGGGTTCAGTTTAATGATGGTCCAGTTGGTTGGCAG 2900
Qy      921 AlaGlyValSerSerIleSerTyrThrSerProAsnGlyGlnThrThrArgTyrGlyGlu 940
Db      2901 GCAGGAGTGTCTCTATCAGTTATACCTCACCAAAATGGTCAAAACAACATAGGTATGGAGAA 2960
Qy      941 AsnGluLysLeuProAspTyrIleLysGlnLysLeuGlnCysLeuSerSerIleLeuLeu 960
Db      2961 AATGAAAAATATACAGACTACATCAACACAGAAATTACAGTGTCGTCTTCCATCCTTTTG 3020
Qy      961 MetPheSerAsnProThrProAsnPheHis 970
Db      3021 ATGTTTCTTAATCCGACTCCTTAATTTTCAT 3050

RESULT 6
US-10-887-553A-750
; Sequence 750, Application US/10887553A
; Publication No. US20050085436A1
; GENERAL INFORMATION:
; APPLICANT: Garza, Dan
; APPLICANT: Li, Hao
; TITLE OF INVENTION: Method to treat conditions associated
; with insulin signalling dysregulation
; FILE REFERENCE: 4-33262
; CURRENT APPLICATION NUMBER: US/10/887,553A
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: 60/485,883
; PRIOR FILING DATE: 2003-08-07
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 750
; LENGTH: 3331
; TYPE: DNA
; ORGANISM: human
US-10-887-553A-750

Alignment Scores:
Pred. No.: 0 Length: 3331
Score: 5057.00 Matches: 965
Percent Similarity: 99.79% Conservative: 3
Best Local Similarity: 99.48% Mismatches: 2
Query Match: 99.59% Indels: 0
DB: 21 Gaps: 0

US-10-026-021-2 (1-970) x US-10-887-553A-750 (1-3331)
Qy      1 MetAlaThrCysIleGlyGlyLysIleGluAspPheLysValGlyAsnLeuGlyLys 20
Db      189 ATGGCGACCTGTCATCGGGGAGGAAGATCGAGGATTTTAAAGTTGGAATCTGCTTGTAAA 248
Qy      21 GlySerPheAlaGlyValTyrArgAlaGluSerIleHisThrGlyLeuGluValAlaIle 40
Db      249 GGATCATTTGCTGGTGTCTACAGAGCTGAGTCCATTCACAGTGGTTTGGAAAGTTGCAATC 308
Qy      41 LysMetIleAspLysIleAlaMetTyrLysAlaGlyMetValGlnArgValGlnAsnGlu 60
Db      309 AAAATGATAGATAGAAAGCCCATGTACAAAGCAGGAATGGTACAGAGAGTCCAAATGAG 368
Qy      61 ValLysIleHisCysGlnLeuLysHisProSerIleLeuGluLeuTyrAsnTyrPheGlu 80
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Db      369 GTGAAAATACATTGCCAAATCGAAACATCCTTCTATCTTTGGAGCTTTATAACTATTTTGA 428
Qy      81 AspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsnGlyGluMetAsnArgTyr 100
Db      429 GATAGCAATTAATGATGTTATCTGGTATTAGAAATGTGCCATAATATGGAGAAATGAACAGGTAT 488
Qy      101 LeuLysAsnArgValLysProPheSerGluAsnGluAlaArgHisPheMetHisGlnIle 120
Db      489 CTAAGAAATAGAGTGAACCCCTTCTCAGAAATGAAGCTCGACACTTCATGACCAGATC 548
Qy      121 IleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHisArgAspLeuThrLeuSer 140
Db      549 ATCAGAGGATGTTGTTATCTTCTCATGTTATCTACACCGGAGCTTCACACTTCT 608
Qy      141 AsnLeuLeuLeuThrArgAsnMetAsnIleLysIleAlaAspPheGlyLeuAlaThrGln 160
Db      609 AACCTCCTACTGACTCGTAATATGAACATCAAGATTGCTGATTTTGGCTGGCACTCAA 668
Qy      161 LeuLysMetProHisGluLysHisTyrThrLeuCysGlyThrProAsnTyrIleSerPro 180
Db      669 CTGAAAATGCCACATGAAAGCACTATACATTATGTGGAACCTCTTAATCTACATTTTCA 728
Qy      181 GluIleAlaThrArgSerAlaHisGlyLeuGluSerAspValTrpSerLeuGlyCysMet 200
Db      729 GAAATGGCACTCGAAGTGCACATGGCTTGAATCTGATGTTTGGTCCCTGGGCTGTATG 788
Qy      201 PheTyrThrLeuLeuIleGlyArgProPheAspThrAspThrValLysAsnThrIleu 220
Db      789 TTTTATACATTACTTATCGGGAGACCACCTTCGACACTGCACAGTCAAGAACACATTA 848
Qy      221 AsnLysValValLeuAlaAspTyrGluMetProSerPheLeuSerIleGluAlaLysAsp 240
Db      849 AATAAAGTAGTATTGGCAGATTATGAATGCCAATCTTTTGTCAATAGAGGCCAAGGAC 908
Qy      241 LeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeuSerLeuSerSerValLeu 260
Db      909 CTTATTCACCAGTTACTTCGTAGAAATCCACAGACATCGTTAAGTCTGCTCTCAGTATTG 968
Qy      261 AspHisProPheMetSerArgAsnSerSerThrLysSerLysAspLeuGlyThrValGlu 280
Db      969 GACCATCCTTTTATGTCCTCGAAATTTCTCAACAAAAAGTAAAGATTTAGGAACCTGTG 1028
Qy      281 AspSerIleAspSerGlyHisAlaThrIleSerThrAlaIleThrAlaSerSerSerThr 300
Db      1029 GACTCAATTGATAGTGGCATGCCACAATTTCTACTGCAATTACAGCTTCTTCCAGTACC 1088
Qy      301 SerIleSerGlySerLeuPheAspLysArgArgLeuLeuIleGlyGlnProLeuProAsn 320
Db      1089 AGTATAAGTGTAGTTTATTGTGACAAAAGAGACTTTTGTATTTGTCAGCCACTCCCAAT 1148
Qy      321 LysMetThrValPheProLysAsnLysSerSerThrAspPheSerSerSerSerGlyAspGly 340
Db      1149 AAAATGAGTGTATTTCCAAGAAATAAAAGTTTCAACTGATTTTCTTCTTCAGGAGATGGA 1208
Qy      341 AsnSerPheTyrThrGlnTrpGlyAsnGlnGluThrSerAsnSerGlyArgGlyArgVal 360
Db      1209 AACAGTTTTTATCTCAGTGGGGAATCAAGAAACCAGTAATAGTGAAGGGGAAGAGTA 1268
Qy      361 IleGlnAspAlaGluGluArgProHisSerArgTyrLeuArgArgAlaTyrSerSerAsp 380
Db      1269 ATTCAAGATGCAGAAAGAAAGGCCACATTTCTCGATACCTTCTGTAGAGCTTATTCTCTGAT 1328
Qy      381 ArgSerGlyThrSerAsnSerGlnSerGlnAlaLysThrTyrThrMetGluArgCysHis 400
Db      1329 AGATCTGCACCTTCTTAATAGACAGTCTCAAGCAAAAAACATATACAATGAACAGATGTCAC 1388
Qy      401 SerAlaGluMetLeuSerValSerLysArgSerGlyGlyGlyGluAsnGluGluArgTyr 420
Db      1389 TCACAGAAATGCTTTTCAGTGTCCAAAGATCAGAGGAGGTGAAATGAAGAGAGGTAC 1448
Qy      421 SerProThrAspAsnAsnAlaAsnIlePheAsnPhePheLysGluLysThrSerSerSer 440
Db      1449 TCACCCACAGACAACAATGCCAACATTTTAACTTCTTTAAAGAAAAAGACATCCAGTAGT 1508
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QY 441 SerGlySerPheGluArgProAspAsnAenGlnAlaLeuSerAsnHisLeuCysProGly 460
DB 1509 TCTGGATCTTTTGAAGAGCCTGATACCAATCAAGCACTCTCCAATCATCTTTGTCCAGGA 1568
QY 461 LysThrProPheProPheAlaAspProThrProGlnThrGluThrValGlnGlnTrpPhe 480
DB 1569 AAAACTCTCTTTTCCATTTTGCAGACCCGACCACTTCAGACTGAAACCGTACACAGTGGTTT 1628
QY 481 GlyAsnLeuGlnIleAsnAlaHisLeuArgLysThrThrGluTyAspSerIleSerPro 500
DB 1629 GGGATCTGCAATAATAATCTCAATTAAGAAAACTTACTGAATATGACAGCATCAGCCCA 1688
QY 501 AsnArgAspPheGlnGlyHisProAspLeuGlnLysAspThrSerLysAsnAlaTrpThr 520
DB 1689 AACCGGAGCTTCAGGGCCATCCAGATTTGCAGAGGACACATCAAAAAATGCCCTGGACT 1748
QY 521 AspThrLysValLysLysAsnSerAspAlaSerAspAsnAlaHisSerValLysGlnGln 540
DB 1749 GATACAAAAGTCAAAAGAACTCTGATGCTTCTGATAATGCGACATTTCTGTAAACAGCA 1808
QY 541 AsnThrMetLysThrMetThrAlaLeuHisSerLysProGluIleLeuGlnGlnCys 560
DB 1809 AATACCATGAATATATGACTGCACTTCACAGTAACCTGAGATTAATCCACAGAAATGT 1868
QY 561 ValPheGlySerAspProLeuSerGluGlnSerLysThrArgGlyMetGluProTrp 580
DB 1869 GTTTTGGCTCAGATCTCTTCTGAAACAGAGCAAGACTAGGGGTATGGAGCCACCATGG 1928
QY 581 GlyTyGlnAsnArgThrLeuArgSerIleThrSerProLeuValAlaHisArgLeuLys 600
DB 1929 GGTATATCAAGATCGTACATTAAGAGCAATATCATCTCCGTTGGTTGCTCACAGGTAA 1988
QY 601 ProfileArgGlnLysThrLysLysAlaValValSerIleLeuAspSerGluGluValCys 620
DB 1989 CCNATCACAGACAAAACCAAAAGGCTGTGGTACACATCTTGATTCAGAGGAGGTGT 2048
QY 621 ValGluLeuValLysGluTyAlaSerGlnGluTyValLysGluValLeuGlnIleSer 640
DB 2049 GTGGAGCTGTGAAGAGATGATGCATCTCAAGAAATATGTGAAGAAAGTTCTTTCAGATACT 2108
QY 641 SerAspGlyAsnThrIleThrIleTyTyProAsnGlyGlyArgGlyPheProLeuAla 660
DB 2109 AGTGATGAAATPACCATCACTATTATTATATCCAAATGGTGTGAGAGGTTTCTCTTGT 2168
QY 661 AspArgProProSerProThrAspAsnIleSerArgTySerPheAspAsnLeuProGlu 680
DB 2169 GATAGACCACTTCCCTACTGACAAATCAGTAGTACAGCTTTGACAAATTTACAGAA 2228
QY 681 LysTyTrpArgLysTyGlnTyAlaSerArgPheValGlnLeuValArgSerLysSer 700
DB 2229 AAATACTGGCGAAATATCAATATGCTTCCAGGTTTGTACAGCTTCTAAGATCTAAATCT 2288
QY 701 ProLysIleThrTyPheThrArgTyAlaLysCysIleLeuMetGluAsnSerProGly 720
DB 2289 CCCAAATCACTTATTTTACAGATATGCTAAATGCAATTTTGTATGGAGAAATCTCCTGGT 2348
QY 721 AlaAspPheGluValTrpPheTyArgGlyValLysIleHisLysThrGluAspPheIle 740
DB 2349 GCTGATTTTGGGTTTGGTTTATGATGGGGTAAATAATACAAACAGAGATTTTCATT 2408
QY 741 GlnValIleGluLysThrGlyLysSerTyThrLeuLysSerGluSerGluValAsnSer 760
DB 2409 CAGGTGATGTAAGACAGAGGAGTCTTACACTTTAAAAAGTGAAGTGAAGTTAATAGC 2468
QY 761 LeuLysGluGluIleLysMetTyMetAspHisAlaAsnGluGlyHisArgIleCysLeu 780
DB 2469 TTGAAAGAGGAGATAAAAATGATATGACCATGCTAATGAGGTCATCGTATTGTTTA 2528
QY 781 AlaLeuGluSerIleIleSerGluGluArgLysThrArgSerAlaProPhePro 800
DB 2529 GCATGGGAATCCATAATTTCAAGAGGAAAGGAAACCTAGGAGTGCCTCCCTTTTCCCA 2588
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QY 801 IleIleIleGlyArgLysProGlySerThrSerSerProLysAlaLeuSerProPro 820
DB 2589 ATAATCATAGGAAGAAAACCTGGTAGTACTAGTTTACCTTAAGGCTTATCACCTCTCT 2648
QY 821 SerValAspSerAsnTyProThrArgAspArgAlaSerPheAsnArgMetValMetHis 840
DB 2649 TCTGTGGATTCAAAATTTACCAACGAGATGAGCATCTTTTCAACAGAAATGTCATGCAT 2708
QY 841 SerAlaAlaSerProThrGlnAlaProIleLeuAsnProSerMetValThrAsnGluGly 860
DB 2709 AGTGATGCTTCTCCAACACAGGCCCAATCCTTAATCCTCTATGTTTACAAATGAAGA 2768
QY 861 LeuGlyLeuThrThrAlaSerGlyThrAspIleSerSerAsnSerLeuLysAspCys 880
DB 2769 CTTGGTCTTCAAACTACAGCTTCTGGAACAGACATCTCTTCTAAATAGTCTAAAAGATTGT 2828
QY 881 LeuProLysSerAlaGlnLeuLysSerValPheValLysAsnValGlyTrpAlaThr 900
DB 2829 CTTCTTAATCAGCAAACTTTTGAATCTGTGTTTGTGAAAAATGTTGGTTGGGCTACA 2888
QY 901 GlnLeuThrSerGlyValAlaValTrpValGlnPheAsnAspGlySerGlnLeuValValGln 920
DB 2889 CAGTTAACTAGTGAGCTGTGTGGTTCAGTTTAATGATGGTCCAGTTCGTTGTGCAG 2948
QY 921 AlaGlyValSerSerIleSerTyThrSerProAsnGlyGlnThrArgTyGlyGlu 940
DB 2949 GCAGAGTGTCTTCTATCAGTTATACCTTCAACAAATGGTCAACAACTAGGTATGAGAA 3008
QY 941 AsnGluLysLeuProAspTyIleLysGlnLysLeuGlnCysLeuSerSerIleLeuLeu 960
DB 3009 AATGAAAAATTTACCAGACTACATCAACAGAAAAATTACAGTGTCTGTCTTCCATCTTTTG 3068
QY 961 MetPheSerAsnProThrProAsnPheHis 970
DB 3069 ATGTTTCTAATCCGACTCCTTAATTTTCAT 3098
RESULT 7
US-10-425-114-26254
; Sequence 26254, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26254
; LENGTH: 2836
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4119-112-B4_FLI
US-10-425-114-26254
Alignment Scores:
Pred. No.: 0 Length: 2836
Score: 4861.00 Matches: 927
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.89% Mismatches: 0
Query Match: 95.73% Indels: 0
DB: 18 Gaps: 0
US-10-026-021-2 (1-970) x US-10-425-114-26254 (1-2836)
QY 43 IleAspLysLysAlaMetTyLysAlaGlyMetValGlnArgValGlnAsnGluValLys 62
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Db 2 ATAGATAGAAAGACCATGTCAAAACGAGGAATGGTACAGAGAGTCCAAAATGAGGTGAA 61  
Qy 63 lleHisCysGlnLeuLysHisProSerIleLeuGluLeuTyrAsnTyrPheGluAspSer 82  
Db 62 ATACATTGCCAATTGAACATCCTTCTATCTTGAGAGCTTATAACTATTTTGAAGATAGC 121  
Qy 83 AsnTyrValTyrLeuValLeuGluMetCysHisAsnGlyGluMetAsnArgTyrLeuLys 102  
Db 122 AATTATGTGTATCTGGTATTAGAAATGGCCATAATGGAGAAATGAAACAGGTATCTAAG 181  
Qy 103 AsnArgValLysProPheSerGluAsnGluAlaArgHisPheMetHisGlnIleIleThr 122  
Db 182 AATAGAGTGAACCCCTTCTCAGAAATGAAGCTCGACACTTCATGCACCATCATCACA 241  
Qy 123 GlyMetLeuTyrLeuHisSerHisGlyIleLeuHisArgAspLeuThrLeuSerAsnLeu 142  
Db 242 GGGATGTTGTATCTTCATTCTCATGGTATATCTACACCGGAGCCTCACACTTCTTAACCTC 301  
Qy 143 LeuLeuThrArgAsnMetAsnIleLysIleAlaAspPheGlyLeuAlaThrGlnLeuLys 162  
Db 302 CTACTGACTCGTAATATGAACATCAAGATTGCTGATTTTGGGCTGGCAACTCAACTGAAA 361  
Qy 163 MetProHisGluLysHisTyrThrLeuCysGlyThrProAsnTyrIleSerProGluIle 182  
Db 362 ATGCCACATGAAGACCATATACATTATGTGGAATCTCTAACTACATTTCCACGAAATT 421  
Qy 183 AlaThrArgSerAlaHisGlyLeuGluSerAspValTyrPheLeuGlyCysMetPheTyr 202  
Db 422 GCCACTCGAAGTGCACATGGCCCTTGAATCTGATGTTGGTCCCTGGGCTGATGTTTAT 481  
Qy 203 ThrLeuLeuIleGlyArgProPheAspThrArgPheThrValLysAsnThrLeuAsnLys 222  
Db 482 ACATTACTTATCGGAGAGCACCCCTTCGACACTGCACAGTCAAGAACACATTAATAATAA 541  
Qy 223 ValValLeuAlaAspTyrGluMetProSerPheLeuSerIleGluAlaLysAspLeuIle 242  
Db 542 GTAGTATTGGCAGATTGAATGCCATCTTTTGTCAATAGAGGCCAAGGACCTTATT 601  
Qy 243 HisGlnLeuLeuArgArgAsnProAlaAspArgLeuSerLeuSerSerValIleAspHis 262  
Db 602 CACCAAGTTACTTTCGTAGAAATCCAGCAGATCGTTTAAAGTCTGCTTCAGTATTGGACCAT 661  
Qy 263 ProPheMetSerArgAsnSerSerThrLysSerLysAspLeuGlyThrValGluAspSer 282  
Db 662 CTTTTATGTCCCGAAATCTTCAACAAAAGTAAGATTTAGGAACCTGTGGAAGACTCA 721  
Qy 283 IleAspSerGlyHisAlaThrIleSerThrAlaIleThrAlaSerSerSerThrSerIle 302  
Db 722 ATTGATAGTGGGCATGCCACAATTTCTACTGCAATTCACAGCTTCTTCCAGTACCAGTATA 781  
Qy 303 SerGlySerLeuPheAspLysArgArgLeuLeuIleGlyGlnProLeuProAsnLysMet 322  
Db 782 AGTGTAGTATTATTTGACAAAAGAAAGACTTTTGAATTGGTTCAGCCACTCCCAATAAATAATG 841  
Qy 323 ThrValPheProLysAsnLysSerSerThrAspPheSerSerSerGlyAspGlyAsnSer 342  
Db 842 ACTGTATTCCAAAGAAATAAAGTTCAACTGATTTTCTTTCAGGAGATGGAAACAGT 901  
Qy 343 PheTyrThrGlnTrpGlyAsnGlnGluThrSerAsnSerGlyArgGlyArgValIleGln 362  
Db 902 TTTTATACTCAGTGGGAAATCAAGAACCCAGTATAGTGGAGGGGAGAGTAAATTCAA 961  
Qy 363 AspAlaGluLysProHisSerArgTyrLeuArgArgAlaTyrSerSerAspArgSer 382  
Db 962 GATGCAGAAAGAAAGGCCAATTTCTCGATACCTTCGTAGAGCTTATTCCTCTGATAGATCT 1021  
Qy 383 GlyThrSerAsnSerGlnSerGlnAlaLysThrTyrThrMetGluArgCysHisSerAla 402  
Db 1022 GGCATCTTAAATAGTCAGTCTCAAGCAAAAACATATACAAATGGAACGATGTCACCTCAGA 1081  
Qy 403 GluMetLeuSerValSerLysArgSerGlyGlyGlyGluAsnGluGluArgTyrSerPro 422  
Db 1082 GAAATGCTTTTCAAGTGTCCAAAGATCAGGAGGAGGTGAAATGAAGAGAGGTACTCACCC 1141

Qy 423 ThrAspAsnAsnAlaAenIlePheAsnPhePheLysGluLysThrSerSerSerSerGly 442  
Db 1142 ACAGACAAACATGTCACCATTTTTTAACTTCTTTAAAGAAAGACATCAGTAGTTCTGGA 1201  
Qy 443 SerPheGluArgProAspAsnAsnGlnAlaLeuSerAsnHisLeuCysProGlyLysThr 462  
Db 1202 TCTTTTGAAGACCTGATTAACAATCAAGCACTCTCCAATCATCTTTGTCCAGGAAAACCT 1261  
Qy 463 ProPheProPheAlaAspProThrProGlnThrGluThrValGlnGlnTrpPheGlyAsn 482  
Db 1262 CCTTTTCCATTTGTCAGACCCGACACCTCAGACTGAAACCGTACAAACAGTGGTTGGGAAT 1321  
Qy 483 LeuGlnIleAsnAlaHisLeuArgLysThrThrGluTyrAspSerIleSerProAsnArg 502  
Db 1322 CTGCAATAAATGCTCATTTTAAAGAAAAAATACTGAATATGACAGCATCAGCCCAACCGG 1381  
Qy 503 AspPheGlnGlyHisProAspLeuGlnLysAspThrSerLysAsnAlaTyrThrAspThr 522  
Db 1382 GACTTCCAGGCCCATCCAGATTTCAGAGAGACATCAAAAAAATGCTTGAGACTGATACA 1441  
Qy 523 LysValLysLysAsnSerAspAlaSerAspAsnAlaHisSerValLysGlnGlnAsnThr 542  
Db 1442 AAAGTCAAAAAGAACTCTGATGCTTCTGATAATGSCACATCTCTGTAACACCAAAATACC 1501  
Qy 543 MetLysTyrMetThrAlaLeuHisSerLysProGluIleIleGlnGlnGluCysValPhe 562  
Db 1502 ATGAAATATATGACTGCACTTTCACAGTAAACCTGAGATAATCCAACAAAGATGTGTTTT 1561  
Qy 563 GlySerAspProLeuSerGluGlnSerLysThrArgGlyMetGluProProTyrGlyTyr 582  
Db 1562 GGCTCAGATCTCTTCTGAAACAGAGCAAGACTAGGGGTATGGAGCCACCACCATGGGTTAT 1621  
Qy 583 GlnAsnArgThrLeuArgSerIleThrSerProLeuValAlaHisArgLeuLysProIle 602  
Db 1622 CAGAACTGATTAAGAGCAATTACATCTCCGTTGGTTGCTTCACAGGTTAAACCAATC 1681  
Qy 603 ArgGlnLysThrLysLysAlaValSerIleLeuAspSerGluGluValCysValGlu 622  
Db 1682 AGACAGAAAAACCAAAAGGCTGTGTGAGCATACTTGATTCAGAGAGAGGTGTGTGGAG 1741  
Qy 623 LeuValLysGluTyrAlaSerGlnGluTyrValLysGluValLeuGlnIleSerSerAsp 642  
Db 1742 CTTGTAAAGGATGATGATCTCAAGAAATATGTGAAGAGATTCTTCAGATATCTAGTAT 1801  
Qy 643 GlyAsnThrIleThrIleTyrTyrProAsnGlyGlyArgGlyPheProLeuAlaAspArg 662  
Db 1802 GGAATAACGATCACTATTATTATCCAAATGGTGTAGAGGTTTTCTCTTGTGTATAGA 1861  
Qy 663 ProProSerProThrAspAsnIleSerArgTyrSerPheAspAsnLeuProGluLysTyr 682  
Db 1862 CCACCCCTCACCTACTGCAACATCAGTAGGTACAGCTTTTGACAAATTTTACCAGAAAAATAC 1921  
Qy 683 TrpArgLysTyrGlnTyrAlaSerArgPheValGlnLeuValArgSerLysSerProLys 702  
Db 1922 TGGCGAAAATATCAATATGCTTCCAGGTTTGTCAGCTTGTAAATCTTAAATCTCCCAA 1981  
Qy 703 IleThrTyrPheThrArgTyrAlaLysCysIleLeuMetGluAsnSerProGlyAlaAsp 722  
Db 1982 ATCACTTATTTTTCAAGATATGCTAAATGCAATTTTGTGGAGAAATTCCTCGTGTCTGAT 2041  
Qy 723 PheGluValTrpPheTyrAspGlyValLysIleHisLysThrGluAspPheIleGlnVal 742  
Db 2042 TTTGAGGTTTGGTTTTATGATGGGGTAAAAATACACAAAACAGAAAGATTTTCATTTCAGGTG 2101  
Qy 743 IleGluLysThrGlyLysSerTyrThrLeuLysSerGluSerGluValAsnSerLeuLys 762  
Db 2102 ATTGAAAAGACAGGGAAGTCTTACACTTTAAAAAGTGAAGTGAAGTTAATAGCTTGAAA 2161  
Qy 763 GluGluIleLysMetTyrMetAspHisAlaAsnGluGlyHisArgIleCysLeuAlaLeu 782  
Db 2162 GAGGAGATAAAAAATGATATGAGCACCATGCTAATGAGGGTCACTGATTTTGTATTAGCACTG 2221





Db 1369 AATTCAAGATGCAGAAAGGCCACATCTTCGATACCTTCGTAGAGCTTATTCCTCTGA 1428  
QY 380 pARSerGlyThrSerAsnSerGlnSerGlnAlaLysThrTyrThrMetGluArgCysHi 400  
Db 1429 TAGATCTGGCAGCTTCTAATAGTTCAGTCTCAAGCAAAAACATATACAATGAACGATGTCA 1488  
QY 400 sSerAlaGluMetLeuSerValSerLysArgSerGlyGlyGlyGluAsnGluArgTyr 420  
Db 1489 CTCAGCAGAAATGCTTTTCAGTGTCCAAAGATCAGAGAGGTGAAATGAAGAGAGTGA 1548  
QY 420 rSerProThrAspAsnAsnAlaAsnIlePheAsnPhePheLysGluLysThrSerSerSe 440  
Db 1549 CTCACCCACAGACAACATGCCAACATTTTAACTTCTTTAAAGAAAAGACATCCAGTAG 1608  
QY 440 rSerGlySerPheGluArgProAspAsnAsnGlnAlaLeuSerAsn-HisLeuCysProG 460  
Db 1609 TTCTGGATCTTTTGAAGACCTGATAACAATCAAGCACTCTCCAATGCATCTTTGTCCAG 1668  
QY 460 lYlvsThrProPheProPheAlaAspProThrProGlnThrGluThrValGlnGlnTrpP 480  
Db 1669 GAAAACCTCTTTTCCATTTGAGACCCGACACCTCAGACTGAAACCGGTACAACAGTGGT 1728  
QY 480 heGlyAsnLeuGlnIleAsnAlaHisLeuArgLysThrThrGluTyrAspSerIleSerP 500  
Db 1729 TTGGGAATCTGCAATTAATGCTCATTTAAGAAAACCTACTGAATATGACAGCATCAGCC 1788  
QY 500 roAsnArgAspPheGlnGlyHisProAspLeuGlnLysAspThrSerLysAsnAlaTrpT 520  
Db 1789 CAAACCGGAGCTTCCAGGCGCATCCAGATCTTCAGAAAGACACATCAAAAAATGCTGGA 1848  
QY 520 hrAspThrLysValLysLysAsnSerAspAlaSerAspAsnAlaHisSerValLysGlnG 540  
Db 1849 CTGATACAAAAGTCAAAAAGAACTCTGATGCTTCTGATAATGCACATTTCTGFAAAACAGC 1908  
QY 540 InAsnThrMetLysTyrMetThrAlaLeuHisSerLysProGluIleIleGlnGlnGluC 560  
Db 1909 AAAATACCATGAAATATATGACTGCACCTTCACAGTAAACCTGAGATATATCCNACAAGAT 1968  
QY 560 yValPheGlySerAspProLeuSerGluGlnSerLysThrArgGlyMetGluProProT 580  
Db 1969 GTGTGTTTTGGCTCAGATCTCTTTCTGAACAGCAAGACTAGGGGTATGAGCCACCAT 2028  
QY 580 rGlyTyrGlnAsnArgThrLeuArgSerIleThrSerProLeuValAlaHisArgLeuL 600  
Db 2029 GGGGTATCAGAAATCGTACATTAAGAAGCATTTACATCTCCGTTGCTGTCTCACAGTTAA 2088  
QY 600 ySProIleArgGlnLysThrLysLysAlaValValSerIleLeuAspSerGluGluValC 620  
Db 2089 AACCAATCAGACAGAAAACCAAAAGGCTGTGTGAGCATACTTGAATTCAGAGGAGTGT 2148  
QY 620 yValGluLeuValLysGluTyrAlaSerGlnGluTyrValLysGluValLeuGlnIleS 640  
Db 2149 GTGTGGAGCTTGTAAAGGAGTATGCATCTCAAGAAATATGTGAAGAAAGTTCTTCAGATAT 2208  
QY 640 erSerAspGlyAsnThrIleThrIleTyrTyrProAsnGly-GlyArgGlyPheProLeu 659  
Db 2209 CTAGTGATGGAATACGATCACTATTATTTATCCAAATGGTGGGTAGAGGTTTCCCTCTT 2268  
QY 660 Ala-AspArgProProSerProThr-AspAsnIleSerArgTyrSerPheAspAsnLeuP 679  
Db 2269 GCTGGATAGACCAACCTCACCTACTTGCACACATCAGTAGGTACAGCTTTGACAAATTTAC 2328  
QY 679 roGluLysTyrTrpArgLysTyrGlnTyrAlaSerArgPheValGlnLeuValArgSerL 699  
Db 2329 CAGAAAAATACCTGGCGAAAAATATCAATATGCTTCCAGGTTTGTACAGCTTGTAAAGATCTA 2388  
QY 699 ySerProLysIleThrTyrPheThrArgTyrAlaLysCysIleLeuMetGluAsnSerP 719  
Db 2389 AATCTCCCAAAATCACTTATTTTACAAGATATGCTAAATGCAATTTGATGAGAAATCTC 2448  
QY 719 roGlyAlaAspPheGluValTrpPheTyrAspGlyValLysIleHisLysThrGluAspP 739

Db 2449 CTGTGCTGATTTTGGAGTGTGGTTTTATGATGGGTAAAAATACAAAAACAGAGATT 2508  
QY 739 heIleGlnValIleGluLysThrGlyLysSerTyrThrLeuLysSerGluSerGluValAla 759  
Db 2509 TCATTCCAGTGATTTGMAAAGACAGGAAGTCTTACACTTTTAAAAAGTGAAGTTA 2568  
QY 759 snSerLeuLysGluGluIleLysMetTyr-MetAspHisAlaAsn-GluGlyHisArgIle 778  
Db 2569 ATAGCTTGAAGAGAGAGATAAAAAATGTATAATGGACCATGTCTAATGGAGGGTCACTCGTAT 2628  
QY 778 eCysLeuAlaLeuGluSerIleIleSerGluGluGluArgLysThrArgSerAlaProPh 798  
Db 2629 TTGTTTAGCACTGGAAATCCATAATTTCCAGAGAGGAAGAAACTAGAGGTGCTCCCTT 2688  
QY 798 ePheProIleIleLysArgLysProGly-SerThrSerSerProLysAlaLeuSerP 818  
Db 2689 TTTCCCAATAATCATAGGAAGAAACCTGTGTGAGTACTAGTTCCACTAAGGCTTTATCAC 2748  
QY 818 roProProSer-ValAspSerAsnTyrProThrArgAspArgAlaSerPheAsnArgMet 837  
Db 2749 CTCCTCTCTTCTGTGGATTTCAAAATTACCCAACGAGAGATAGAGCATCTTTCAACAGAATG 2808  
QY 838 ValMethHisSerAlaAlaSerProThrGlnAlaProIleLeuAsnProSerMetValThr 857  
Db 2809 GTCATGCATAGTGTGCTTCTCCAACACAGGACCAATCCTTAATCCCTCTATGGTTACA 2868  
QY 858 AsnGluGlyLeuGlyLeuThrThrAlaSerGlyThr-AspIleSerSerAsnSerLys 877  
Db 2869 AATGAAGGACTTGGTCTTACCACTACAGGTTTTGGGACGACGACATCTCTTCTAATAGTCT 2928  
QY 877 uLysAspCysLeuPro---LysSerAlaGlnLeuLysSer-ValPheValLysAsn- 895  
Db 2929 AAAAGATGTCTTCTCTATAATACGCGACCACTTTTGAAATCTCGTTTTGTGAAAAAT 2988  
QY 896 --ValGlyTrpAla---ThrGlnLeuThrSerGlyAlaValTrpValGlnPheAsnAspG 914  
Db 2989 GTTTGGTTGGGCATACCACGTTAACTAGTGAGCTGTGTGGTTGAGTTTAAATGATG 3048  
QY 914 lYSerGlnLeuValValGlnAla-GlyValSerSer-IleSerTyrThrSerProAsnGln 933  
Db 3049 GGTCACAGTTGGTGTGCGAGGACAGAGTGTCTTCAACAAGTTATACCTCACCAGATGG 3108  
QY 933 yGlnThr-ThrArgTyrGlyGluAsnGluLysLeuProAspTyrIleLysGlnLysLeuG 953  
Db 3109 TCAAAACCACTAGTATGAGGAAAAATGAAAAATTTACCGGACTACATCAACAGAAATTAC 3168  
QY 953 InCysLeuSerSerIleLeuLeuMetPheSerAsnProThrProAsnPheHis 970  
Db 3169 AGTGTCTGTCTCCATCTTTTGATGTTTCTAATCCGACTCTCTAATTTTTCAT 3221

## RESULT 9

US-09-918-995-21560  
; Sequence 21560, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; PRIORITY FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIORITY FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 21560  
; LENGTH: 484  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(484)  
; OTHER INFORMATION: n = A,T,C or G

## US-09-918-995-21560

Alignment Scores:  
Pred. No.: 2,26e-61 Length: 484  
Score: 743.00 Matches: 142  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 14.63% Indels: 0  
DB: 10 Gaps: 0

## US-10-026-021-2 (1-970) x US-09-918-995-21560 (1-484)

Qy 676 AsnAlaTrpThrPheGlyAsnLeuGlnIleAsnAlaHisLeuArgLysThrGluTyrAsp 695  
Db 59 GACATATTTACAGAAAATACTGGCGAAAATATCAATATGCTTCAGGTTTGTACAGCTT 118  
Qy 696 ValArgSerLysSerProLysIleThrTyrPheThrArgTyrAlaLysCysIleLeuMet 715  
Db 119 GTAAGATCTAATCTCCCAATACATTTATTTTACAGATATGCTTAATGCAATTTTGTATG 178  
Qy 716 GluAsnSerProGlyAlaAspPheGluValTrpPheTyrAspGlyValLysIleHisLys 735  
Db 179 GAGAATCTCTGGTCTGATTTTGAGGTTTGTATGATGGGTAAAAATACACAAA 238  
Qy 736 ThrGluAspPheIleGlnValIleGluLysThrGlyLysSerTyrThrLeuLysSerGlu 755  
Db 239 ACAGAAGATTTCAATTCAGGTGATTTGAAAAGACAGCGAAGTCTTACACTTTAAAAAGTGA 298  
Qy 756 SerGluValAsnSerLeuLysGluLysIleLysMetTyrMetAspHisAlaAsnGluGly 775  
Db 299 AGTGAAGTTATAGCTTGAAGAGAGAGATAAAATGATATGGACCATGCTTAATGAGGGT 358  
Qy 776 HisArgIleCysLeuAlaLeuGluSerIleLeuSerGluGluGluArgLysThrArgSer 795  
Db 359 CATCGTATTTGTTAGCACTGGAATCCATATTTTCAGAGAGAGAAAGAACTAGGAGT 418  
Qy 796 AlaProPhePheProIleIleIleGlyArgLysProGlySerThrSerSerProLysAla 815  
Db 419 GCTCCCTTTTCCCAATAATCATAGGAAGAAACCTGCTAGTACTAGTTCACTAAGGCC 478  
Qy 816 LeuSer 817  
Db 479 TTATCA 484

## RESULT 10

US-09-878-178-96  
; Sequence 96 Application US/09878178  
; Patent No. US2002017552A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Secretist, Heather  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.527  
; CURRENT APPLICATION NUMBER: US/09/878,178  
; NUMBER OF SEQ ID NOS: 2337  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 96  
; LENGTH: 328  
; TYPE: DNA  
; ORGANISM: Homo sapien

## US-09-878-178-96

Alignment Scores:  
Pred. No.: 2,44e-47 Length: 328  
Score: 594.00 Matches: 109  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 11.70% Indels: 0  
DB: 9 Gaps: 0

## US-10-026-021-2 (1-970) x US-09-878-178-96 (1-328)

Qy 477 GlnGlnTrpPheGlyAsnLeuGlnIleAsnAlaHisLeuArgLysThrGluTyrAsp 496  
Db 2 CAACAGTGGTTTGGGAATCTGCAATAAATGCTCATTTAAGAAAACTACTGAATATGAC 61  
Qy 497 SerIleSerProAsnArgAspPheGlnGlyHisProAspLeuGlnLysAspThrSerLys 516  
Db 62 AGCATCAGCCCAACCCGGGACTTCCAGGGCCATCCAGATTTTGCAGAGAGACACATCAAAA 121  
Qy 517 AsnAlaTrpThrAspThrLysValLysValLysValLysValLysValLysValLysValLys 536  
Db 122 AATGCTTGGACTGATACAAAAGTCAAAAAGAACTCTGATGCTTCTGATTAATGACATTTCT 181  
Qy 537 ValLysGlnGlnAsnThrMetLysTyrMetThrAlaLeuHisSerLysProGluIleIle 556  
Db 182 GTAAACACAGCAAAATACCATGAATATATGATGCTGCTTTCACAGTAAACCTGAGATAATC 241  
Qy 557 GlnGlnGluCysValPheGlySerAspProLeuSerGluGlnSerLysThrArgGlyMet 576  
Db 242 CAACAAGAATGTGTTTTTGGCTCAGATCCTCTTTCTGAACACAGACAGACTAGGGGTATG 301  
Qy 577 GluProProTrpGlyTyrGlnAsnArg 585  
Db 302 GAGCCACCATGGGTTTATCAGATCGT 328

## RESULT 11

US-10-046-935-96  
; Sequence 96 Application US/10046935  
; Publication No. US20020156011A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Secretist, Heather  
; APPLICANT: Wang, Aijun  
; APPLICANT: Stolk, John A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.527C1  
; CURRENT APPLICATION NUMBER: US/10/046,935  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 2339  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 96  
; LENGTH: 328  
; TYPE: DNA  
; ORGANISM: Homo sapiens

## US-10-046-935-96

Alignment Scores:  
Pred. No.: 2,44e-47 Length: 328  
Score: 594.00 Matches: 109  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 11.70% Indels: 0  
DB: 13 Gaps: 0

## US-10-026-021-2 (1-970) x US-10-046-935-96 (1-328)

Qy 477 GlnGlnTrpPheGlyAsnLeuGlnIleAsnAlaHisLeuArgLysThrGluTyrAsp 496  
Db 2 CAACAGTGGTTTGGGAATCTGCAATAAATGCTCATTTAAGAAAACTACTGAATATGAC 61  
Qy 497 SerIleSerProAsnArgAspPheGlnGlyHisProAspLeuGlnLysAspThrSerLys 516  
Db 62 AGCATCAGCCCAACCCGGGACTTCCAGGGCCATCCAGATTTTGCAGAGAGACACATCAAAA 121  
Qy 517 AsnAlaTrpThrAspThrLysValLysValLysValLysValLysValLysValLysValLys 536  
Db 122 AATGCTTGGACTGATACAAAAGTCAAAAAGAACTCTGATGCTTCTGATTAATGACATTTCT 181  
Qy 537 ValLysGlnGlnAsnThrMetLysTyrMetThrAlaLeuHisSerLysProGluIleIle 556

Db 182 GTAAACAGCAAAATACCATGAATATATGACTGCTTCCAGCTTACAGTAAACCTGAGATAATC 241  
QY 557 GlnGlnGluCysValPheGlySerAspProLeuSerGluGlnSerIleThrArgGlyMet 576  
Db 242 CAACAGAAATGTGTTTTGGCTCAGATCCTCTTTCTGAACAGCAAGCAGTAGGGGTATG 301  
QY 577 GluProProTrrpGlyTyrGlnAsnArg 585  
Db 302 GAGCCACCATTGGGTTATCAGAAATCGT 328

## RESULT 12

US-10-146-502-96  
; Sequence 96, Application US/10146502  
; Publication No. US20030069180A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Secretist, Heather  
; APPLICANT: Wang, Aijun  
; APPLICANT: Stolk, John A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: AND DIAGNOSIS OF COLON CANCER  
; CURRENT APPLICATION NUMBER: US/10/146,502  
; CURRENT FILING DATE: 2002-05-14  
; NUMBER OF SEQ ID NOS: 2241  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 96  
; LENGTH: 328  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-146-502-96

Alignment Scores:  
Pred. No.: 2,446-47 Length: 328  
Score: 594.00 Matches: 109  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 11.70% Indels: 0  
DB: 14 Gaps: 0

US-10-026-021-2 (1-970) x US-10-146-502-96 (1-328)

QY 477 GlnGlnTrrpPheGlyAsnLeuGlnIleAsnAlaHisLeuArgLysThrGluTyrAsp 496  
Db 2 CAACAGTGGTTTGGGAATCTGCATAAATAGTCTCAATTAAGAAAAAATCTGAAATATGAC 61  
QY 497 SerIleSerProAsnArgAspPheGlnGlyHisProAspLeuGlnLysAspThrSerLys 516  
Db 62 AGCATCAGCCCAACCGGGACTTCCAGGGCCATCCAGATTTCAGAGAGACACATCAAAA 121  
QY 517 AsnAlaTrrpThrAspThrLysValLysLysAsnSerAspAlaSerAspAsnAlaHisSer 536  
Db 122 AATGCTGGAGCTGATACAAAAGTCAAAAAGAACTCTGATGCTTCTGATAATGCACATTCT 181  
QY 537 ValLysGlnGlnAsnThrMetLysTyrMetThrAlaLeuHisSerLysProGluIleIle 556  
Db 182 GTAAACAGCAAAATACCATGAATATATGACTGCTTCCAGTTCACAGTAAACCTGAGATAATC 241  
QY 557 GlnGlnGluCysValPheGlySerAspProLeuSerGluGlnSerLysThrArgGlyMet 576  
Db 242 CAACAGAAATGTGTTTTGGCTCAGATCCTCTTTCTGAACAGCAAGCAGTAGGGGTATG 301  
QY 577 GluProProTrrpGlyTyrGlnAsnArg 585  
Db 302 GAGCCACCATTGGGTTATCAGAAATCGT 328

## RESULT 13

US-10-108-580-1  
; Sequence 1, Application US/10108580  
; Publication No. US20030077681A1  
; GENERAL INFORMATION:  
; APPLICANT: Cogswell, John

; TITLE OF INVENTION: PLK3 PROTEIN-PROTEIN INTERACTIONS  
; FILE REFERENCE: PU4458  
; CURRENT APPLICATION NUMBER: US/10/108,580  
; CURRENT FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 2169  
; TYPE: DNA  
; ORGANISM: homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (37)..(1860)  
; OTHER INFORMATION:  
US-10-108-580-1

Alignment Scores:  
Pred. No.: 1e-45 Length: 2169  
Score: 590.50 Matches: 115  
Percent Similarity: 57.33% Conservative: 61  
Best Local Similarity: 37.46% Mismatches: 106  
Query Match: 11.63% Indels: 25  
DB: 14 Gaps: 4

US-10-026-021-2 (1-970) x US-10-108-580-1 (1-2169)

QY 15 GlyAsnLeuLeuGlyLysGlySerPheAlaGlyValTyrArgAlaGluSerIleHisThr 34  
Db 112 GGCGCTGTTGGGCAAGGGGGCTTCGCCGCTGCTACGAGGCGCACACAGAGACT 171  
QY 35 GlyLeuGluValAlaIleLysMetIleAspLysLysAlaMetTyrLysAlaGlyMetVal 54  
Db 172 GGCGCGCTACGCTGCAAAAGTCATCCGAGAGCGCGCGCAAGCCCGCATCAGCGC 231  
QY 55 GlnArgValGlnAsnGluValLysIleHisCysGlnLeuLysHisProSerIleLeuGlu 74  
Db 232 GAGAAGATCTTAATGAGATTGAGCTGCACCGAGACCTGCAGACCGCCACATCGTGGCT 291  
QY 75 LeuTyrAsnTyrPheGluAspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsn 94  
Db 292 TTTTCGACCACCTTTTGAGGAGCGTGACAAACATCTACATTTCTTGGAGCTCTGCAGCGA 351  
QY 95 GlyGluMetAsnArgTyrLeuLysAsnArgValLysProPheSerGluAsnGluAlaArg 114  
Db 352 AAGTCCCTGGCCCAACATCTGGAAGGCCCGG---CACACCTGTTGGAGCCAGAGTGGCG 408  
QY 115 HisPheMetHisGlnIleIleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHis 134  
Db 409 TACTACCTGGCGCAGATCTTTCTGGCTCAAGTACTTGCACGAGCGGGCATCTTGAC 468  
QY 135 ArgAspLeuThrLeuSerAsnLeuLeuLeuThrArgAsnMetAsnIleLysIleAlaAsp 154  
Db 469 CGGACCTCAAGTTGGGAAATTTTTCATCACTAGAAACATGGAACATGAAGTGGGGAT 528  
QY 155 PheGlyLeuAlaThrGlnLeuLysMetProHisGluLysHisTyrThrLeuCysGlyThr 174  
Db 529 TTTGGCTGGGCGCCCGGTTGGAGCCTCCGAGGAGGAGAAAGAACCATCTGTGGCACC 588  
QY 175 ProAsnTrrpIleSerProGluIleAlaThrArgSerAlaHisGlyLeuGluSerAspVal 194  
Db 589 CCCAACTATGTGGCTCCAGAAAGTCTGCTGAGACAGGGCCACGGCCCTGAAGCGATGTA 648  
QY 195 TrpSerLeuGlyCysMetPheTyrThrLeuLeuIleGlyArgProProPheAspThrAsp 214  
Db 649 TGGTCACTGGGCTGTGTACATGTCATGTCGCGGAGCCCTCTCCCTTTGAGACGGCT 708  
QY 215 ThrValLysAsnThrLeuAsnLysValValLeuAlaAspTyrGluMetProSerPheLeu 234  
Db 709 GACCTGAAGGAGACGTACCGCTGTCATCAAGCAGAGTTCTACAGCTCCCTGCCGCTC 768  
QY 235 SerIleGluAlaLysAspLeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeu 254  
Db 769 TCACTGCTGCCCGGAGCTCTCGGCCCATCTCTCGGGCCTCACCCCGAGACCGCCC 828

QY 255 SerLeuSerSerValLeuAspHisProPheMetSerArgAsnSerSerThrLysSerLys 274  
Db 829 TCTATTGACCATCTGGCCATGACTTCTTTACCAAG-----867  
QY 275 AspLeuGlyThrValGluAspSerIleAspSerGlyHisAlaThrIleSerThrAlaIle 294  
Db 868 -----GGCTACACCCCGATCGACTC-----CCTATCAGCAGCTGGCGTG 906  
QY 295 ThrAlaSerSerSerThr-----SerIleSerGly 304  
Db 907 ACAGTCCAGACCTGACACCCCCCAACCCAGCTAGGAGTCTGTTGGCCAAAGTTACCAAG 966  
QY 305 SerLeuPheAspLysArgArg 311  
Db 967 AGCCTCTTTGGCAGAAAGAG 987  
RESULT 14  
US-10-204-041-15  
; Sequence 15, Application US/10204041  
; Publication No. US20030176443A1  
; GENERAL INFORMATION:  
; APPLICANT: STEIN-GERLACH, MATTHIAS  
; APPLICANT: SALASSIDIS, KONSTANTINOS  
; APPLICANT: BACHER, GERALD  
; APPLICANT: MULLER, STEFAN  
; TITLE OF INVENTION: Pyridylpyrimidine Derivatives as Effective Compounds Against Prio  
; TITLE OF INVENTION: Infections and Prio Diseases  
; FILE REFERENCE: AXM-007.1P US  
; CURRENT APPLICATION NUMBER: US/10/204,041  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: PCT/EP02/05420  
; PRIOR FILING DATE: 2002-05-16  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 2169  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-204-041-15  
Alignment Scores:  
Pred. No.: 1e-45 Length: 2169  
Score: 590.50 Matches: 115  
Percent Similarity: 57.33% Conservative: 61  
Best Local Similarity: 37.46% Mismatches: 106  
Query Match: 11.63% Indels: 25  
Gaps: 4  
US-10-026-021-2 (1-970) x US-10-204-041-15 (1-2169)  
QY 15 GlyAsnLeuGlyLysGlySerPheAlaGlyValTyrArgAlaGluSerIleHisThr 34  
Db 112 GCGCCCTGTTGGGAAGGGGGCTTCGCCCTGCTACGAGCCCACTGACACAGAGACT 171  
QY 35 GlyLeuGluValAlaIleAspMetIleAspLysLysAlaMetTyrIleAlaGlyMetVal 54  
Db 172 GGCAGCGCTACGCTGTAAAGTCAATCCGAGAGCCGCTGCCCAAGCCGGATCAGCGC 231  
QY 55 GlnArgValGlnAsnGluValLysIleHisCysGlnLeuLysHisProSerIleLeuGlu 74  
Db 232 GAGAGATCCTTAATGAGATTGAGTGCACCCAGACCTGCAGCAGCCACATCTGGCT 291  
QY 75 LeuTyrAsnTyrPheGluAspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsn 94  
Db 292 TTTTCGCCACCACTTTGAGGACGCTGACAACATCTACATTTCTGGAGCTCTGCGCGA 351  
QY 95 GlyGluMetAsnArgTyrLeuLysAsnArgValLysProPheSerGluAsnGluAlaArg 114  
Db 352 AAGTCCCTGGCCCAACATCTGGAAAGCCCGG----CACACCCCTTTGGAGCCAGAGTGGCG 408

QY 115 HisPheMetHisGlnIleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHis 134  
Db 409 TACTACCTGGCGCAGATCTTTTGGCCTCAAGTACTTTGCACGCGCGCATCTTGCAC 468  
QY 135 ArgAspLeuThrLeuSerAsnMetLeuThrArgAsnMetAsnIleLysIleAlaAsp 154  
Db 469 CGGACCTCAAGTTGGGAATTTTTCATCACTGAGACATGGAATGAAGTGGGGAT 528  
QY 155 PheGlyLeuAlaThrGlnLeuLysMetProHisGluLysHisTyrThrLeuCysGlyThr 174  
Db 529 TTTGGCTGGCAGCCCGGTGGAGCTCCGGAGCAGAGGAAGAACACCATCTGTGGCACC 588  
QY 175 ProAsnTyrIleSerProGluIleAlaThrArgSerAlaHisGlyLeuGluSerAspVal 194  
Db 589 CCCAACTATGTGGCTCCAGAAAGTGTCTGAGACAGGGGCCACGGCCCTGAACGGATGTA 648  
QY 195 TrpSerLeuGlyCysMetPheTyrThrLeuLeuIleGlyArgProPheAspThrAsp 214  
Db 649 TGTCACTGGGCTGTGTATGATGCTCTCGGGAGGCCCTCTCTTTGAGACGGCT 708  
QY 215 ThrValLysAsnThrLeuAsnLysValValLeuAlaAspTyrGluMetProSerPheLeu 234  
Db 709 GACCTGAAGGAGACGTACCGCTGCATCAAGCAGGTTCACTACACGCTGCTGCCACGCTC 768  
QY 235 SerIleGluAlaLysAspLeuIleHisGlnLeuLeuArgAsnProAlaAspArgLeu 254  
Db 769 TCACTGCTGCCGCGCAGCTCTCGCGCCCTCTTCGGGCTCACCCGAGACCGCCCC 828  
QY 255 SerLeuSerSerValLeuAspHisProPheMetSerArgAsnSerSerThrLysSerLys 274  
Db 829 TCTATTGACCATCTCGCCCATGACTTCTTTACCAAG-----867  
QY 275 AspLeuGlyThrValGluAspSerIleAspSerGlyHisAlaThrIleSerThrAlaIle 294  
Db 868 -----GGCTACACCCCGATCGACTC-----CCTATCAGCAGCTGGCGTG 906  
QY 295 ThrAlaSerSerSerThr-----SerIleSerGly 304  
Db 907 ACAGTCCAGACCTGACACCCCCCAACCCAGCTAGGAGTCTGTTGGCCAAAGTTACCAAG 966  
QY 305 SerLeuPheAspLysArgArg 311  
Db 967 AGCCTCTTTGGCAGAAAGAG 987  
RESULT 15  
US-10-305-720-1147  
; Sequence 1147, Application US/10305720  
; Publication No. US20040010136A1  
; GENERAL INFORMATION:  
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.  
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressi  
; FILE REFERENCE: PA-0002-1 CON  
; CURRENT APPLICATION NUMBER: US/10/305,720  
; CURRENT FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: 09/016,434  
; PRIOR FILING DATE: 1998-01-30  
; NUMBER OF SEQ ID NOS: 1490  
; SOFTWARE: PERL Program  
; SEQ ID NO 1147  
; LENGTH: 2169  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g1488262  
US-10-305-720-1147  
Alignment Scores:  
Pred. No.: 1e-45 Length: 2169  
Score: 590.50 Matches: 115  
Percent Similarity: 57.33% Conservative: 61  
Best Local Similarity: 37.46% Mismatches: 106  
Query Match: 11.63% Indels: 25

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DB:          17          Gaps:          4
US-10-026-021-2 (1-970) x US-10-305-720-1147 (1-2169)
QY 15 GlyAsnLeuLeuGlyLysGlySerPheAlaGlyValTyrArgAlaGluSerIleHisThr 34
   |||||
Db 112 GCGCGCTTGTGGCAAGGGGGCTTCGCGCGCTGCTACGAGGCCACTGACACAGAGACT 171
QY 35 GlyLeuGluValAlaIleValMetIleAspLysLysAlaMetTyrLysAlaGlyMetVal 54
   |||||
Db 172 GCGACGGCTAGCTGTCAAGTCATCCGACAGCCGCGCTGCGCAAGCGCATCAGCGC 231
QY 55 GlnArgValGlnAsnGluValLysIleHisCysGlnLeuLysHisProSerIleLeuGlu 74
   |||||
Db 232 GAGAGATCCCTAATGAGATTGAGCTGCACCGAGACCTGCGAGCCGCCACATCGTGGCT 291
QY 75 LeuTyrAsnTyrPheGluAspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsn 94
   |||||
Db 292 TTTTCGCACCACTTTGAGGACGCTGACAAACATCTACATTTCTTGGAGCTCTGCAGCCGA 351
QY 95 GlyGluMetAsnArgTyrLeuLysAsnArgValLysProPheSerGluAsnGluAlaArg 114
   |||||
Db 352 AAGTCCCTGGCCCAATCTGGGAAGGCCCGG---CACACCTGTTGGAGCCAGAGTGGCC 408
QY 115 HisPheMetHisGlnIleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHis 134
   |||||
Db 409 TACTACCTGGCGCAGATCTTCTGGCTCAAGTACTTGCACCGCGCGGCATCTTGGCAC 468
QY 135 ArgAspLeuThrLeuSerAsnLeuLeuLeuThrArgAsnMetAsnIleLysIleAlaAsp 154
   |||||
Db 469 CGGACCTCAAGTTGGAAATTTTTCATCTACTGAGAACATGGAACCTGAAGTGGGGAT 528
QY 155 PheGlyLeuAlaThrGlnLeuLysMetProHisGluLysHisTyrThrLeuCysGlyThr 174
   |||||
Db 529 TTTGGCTGGCGCGCGGTGGAGCTCCGGAGAGAGGAAAGAACCATCTGTGGCAC 588
QY 175 ProAsnTyrIleSerProGluIleAlaThrArgSerAlaHisGlyLeuGluSerAspVal 194
   |||||
Db 589 CCCACTATGTGGCTCCAGAGTGTGCTGAGACAGGGCCACGGCCCTGAAGCGGATGTA 648
QY 195 TrpSerLeuGlyCysMetPheTyrThrLeuLeuIleGlyArgProProPheAspThrAsp 214
   |||||
Db 649 TGGTCACTGGGCTGTGTGATGACAGCTGCTCTCGGGAGGCCCTCCCTTTGAGACGGCT 708
QY 215 ThrValLysAsnThrLeuAsnLysValValLeuAlaAspTyrGluMetProSerPheLeu 234
   |||||
Db 709 GACCTGAAGGAGACGTACCGCTGCATCAAGCAGGTTCTACTACGCTGCTGCCAGCCTC 768
QY 235 SerIleGluAlaLysAspLeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeu 254
   |||||
Db 769 TCACCTGCCCTGCCGAGCTCTGCGCGCCATCTTCGGGCTCACCCCGAGACCGCCCC 828
QY 255 SerLeuSerSerValLeuAspHisProPheMetSerArgAsnSerSerThrLysSerLys 274
   |||||
Db 829 TCTATTGACAGATCCTGGCCATGACTTCTTTACCAAG----- 867
QY 275 AspLeuGlyThrValGluAspSerIleAspSerGlyHisAlaThrIleSerThrAlaIle 294
   |||||
Db 868 -----GGCTACACCCCGATCGACTC-----CCTATCAGCAGTGGGTG 906
QY 295 ThrAlaSerSerSerThr-----SerIleSerGly 304
   |||||
Db 907 ACAGTCCCGACACCTGACACCCCCACCCAGCAGTAGAGTCTGTTGGCAAGATTACCAAG 966
QY 305 SerLeuPheAspLysArgArg 311
   |||||
Db 967 AGCCTCTTTGGCAGAAAGAG 987

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